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171.51 17
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APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll III, Eddie
APPLICANT: Carroll Andan
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
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                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-328-111-315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-315-794-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 100.000
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  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
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                                                                                                                                                                                                                               Sequence 315, Application US/09328111 Patent No. 6262333 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-09-328-111-315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-988-687-2 x US-09-328-111-315
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Ratio: 1.000
Percent Similarity: 100.000
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US-09-328-111-315
                                                                                                                                                                                                                  seq_documentation_block:
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LENGTH: 238
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110.24 171.51
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                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
    out_format : pfs
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-111-348-9 -
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-606-789-25
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ptodata/2/1na/5A_COMB.seq:US-08-606-789-9
OM of: US-09-988-687-2 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database: Issued_Patents_NA:*
Database sequences: 351203
Database length: 113238999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search time (sec): 53.500000
                                                                                                                                                                                                                                                                                                                                                                                                                                                Search information block:
Query: US-09-988-687-2
Query length: 826
                                       Date: Mar 30, 2002 12:54
                                                                                                                                             Command line parameters
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us-09-988-687-2.olip2n.rni

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seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-578-551-18
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    Sequence 51, Application Us/09389341
    Patent No. 620803
    Patent No. 620803
    GENERAL INFORMATION:
    APPLICANT: Roberts, Christopher J.
    TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
    TITLE OF INVENTION: DRUGS
    FARLER PAPLICATION NUMBER: US/09/389,341
    CURRENT FILING DATE: 1999-09-02
    SEALLER FILING DATE: 1999-05-21
    NUMBER OF SEQ ID NOS: 72
    SEGTWARE: Patentin Ver. 2.0
    SEQ ID NO 51
    LENGTH: 2517
                                                                                                                                  APPLICANT: Roberts, Christopher J.

TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 9301-053
CURRENT APPLICATION NUMBER: US/09/315,794
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 51
LENGTH: 2517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-389-341-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682 LeuLeulleHisGluAlaThrLeuGlu 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-315-794-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-389-341-51
                          eg_documentation_block:
Sequence 51, Application US/09315794
Patent No. 6197517
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US-09-988-687-2 x US-09-315-794-51
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Ratio: 1.000
Percent Similarity: 100.000
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Percent Similarity: 100.000
                                                                                                                GENERAL INFORMATION:
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No. 5854050o No. 5854050disk of No. 5854050th America, Inc.
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                                                                                                                                                                                                                   APPLICANT: Nielsen, Jack B.
APPLICANT: Dambmann, Claus
TITLE OF INVENTION: An Enzyme with Protease Activity
NUMBER OF SEQUENCES: 34
ADDRESSEE: No. 58540500 No. 5854050disk of No. 5854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,551
FILING DATE: 01-FEB-1996
CLASSIFICATION 0435
PRIOR APPLICATION TAR:
APPLICATION NUMBER: WO 0811/93
FILING DATE: 06-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/02044
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 8.00 Length: 8
Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                           STREET: 405 Lexington Avenue, 64th Floor CITY: New York STATE: New York COUNTRY: United States of America ZIP: 10174-6401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Aspergillus aculeatus
265 ProvalGlyThrAlaAlaIleAla 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 CCTGTTGGCACCGCTGCTATTGCT 137
                                                                                                  APPLICANT: Dalboge, Henrik
APPLICANT: Christgau, Stephan
APPLICANT: Andersen, Lene N.
APPLICANT: KOfod, Lene N.
APPLICANT: Kauppinen, Sakari M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-578-551-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lambiris, Elias J. REGISTRATION NUMBER: 33,728 REFERENCE/DOCKET NUMBER: 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-988-687-2 x US-08-578-551-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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ADDRESSEE: No. 61909050 No. 6190905disk of No. 6190905th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
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                                                                                                                                                                                  APPLICANT: Andersen, Lene N.
APPLICANT: Kofod, Lene V.
APPLICANT: Kauppinen, Sakari M.
APPLICANT: Nielsen, Jack B.
APPLICANT: Dambmann, Claus
APPLICANT: An Enzyme with Protease Activity
NUMBER OF SEQUENCES: 34
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: United States of America
ZIP: 1014 -6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/408,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DALE.
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/578,551
APPLICATION NOBER: US/08/578,551
APPLICATION OI-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-FEB-1996
APPLICATION NUMBER: DK 0811/93
FILING DATE: 06-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/02044
FILING DATE: 19-JAN-1995
ATTORNEY/AGENT INFORMATION:
Sequence 18, Application US/09408257
Patent No. 6190905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-09-408-257-18
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US-09-988-687-2 x US-09-408-257-18
                                                                           GENERAL INFORMATION:
APPLICANT: Dalboge, Henrik
APPLICANT: Christgau, Stephan
APPLICANT: Andersen, Lene N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: No. 59981900 No. 5998190disk of No. 5998190th America, Inc. STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-408-257-18
                                                                                                                                                                                                                                               APPLICANT: Kofod, Lene V
APPLICANT: Kauppinen, Sakari M.
APPLICANT: Nielsen, Jack B
APPLICANT: Dambmann, Claus
TITLE OF INVENTION: An Enzyme with Protease Activity
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/190,982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 95/02044
FILING DATE: 19-JAN-1995
ATTONEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4006.204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Aspergillus aculeatus
US-09-190-982-18
                                  Sequence 18, Application US/09190982
Patent No. 5998190
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/578,551
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US-09-988-687-2 x US-09-190-982-18
                                                                                                                                        APPLICANT: Dalboge, Henrik
APPLICANT: Christgau, Stephan
APPLICANT: Andersen, Lene N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 295 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-482-918-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 0300 Sears Tower, 233 South Wacker Drive CITY: 010cago STATE: 111inois COUNTRY: United States of America 21P: 60606-6402 COMPUTER FEADABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: END PC Compatible OPERATING SYSTEM: PC-0DS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/482,918 FILING DATE: 07-JUN-1995 CLASSIFICATION NUMBER: 36,107 REFERENCE/POCKET UNDER: 36,107 REGISTRATION NUMBER: 36,107 RELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-0300 TELEBRAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: US-09-329-350-30 from: 1
                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 100.000
OTHER INFORMATION: /product= "20K-cellulase"
                                                                                                                                                NAME/KEY: exon
LOCATION: 506..881
: LOCATION: 506..881
US-09-329-350-30
                                                                                                 /product= "20K-cellulase
                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
    sequence 60, Application US/08482918
    Patent No. 6207417
    GENERAL INFORMATION:
    APPLICANT: Zsebo, Krisztina M. APPLICANT: Suggs, Sidney V. APPLICANT: Buggs, Sidney V. APPLICANT: Martin, Francis H. TITLE OF INVENTION: Stem Cell Factor NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-988-687-2 x US-09-329-350-30/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        800 AlaGlyGlyLeuGluAspGlyGlu 807
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELERA: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                              Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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MOLECULE TYPE: protein
                     FEATURE:
NAME/KEY: excn
LOCATION: 1877.435
OTHER INFORMATION:
FEATURE:
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LOCATION: 184..1002
FEATURE:
                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                       APPLICANT: Elovainio, Minna
APPLICANT: Elovainio, Minna
APPLICANT: Joutsjoki, Vesa
APPLICANT: Joutsjoki, Vesa
APPLICANT: Paloheimo, Marja
APPLICANT: Suominen, Pirkko
TITLE OF INVENTION: NOVEL CELLULASES, THE GENES ENCODING THEM AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT AFILICATION DATA:
APPLICATION NUMBER: US/09/329,350
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                               ANUKESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Shea Jr., Timothy
REGISTRATION NUMBER: 41,306
REPERENCE/DOCKET NUMBER: 1716.0510006/MAC/TJS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2560
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/841,636
FILING DATE: 30-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,335
FILING DATE: 17-0CT-1995
FILING DATE: 04-DEC-1995
FILING DATE: 04-DEC-1995
FILING DATE: 28-JUN-1996
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,840
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/732,181
FILING DATE: 16-0CT-1996
FILING DATE: 16-0CT-1996
FILING DATE: 110-0CT-1996
FILING DATE: 110-0CT-1996
FILING DATE: 17-0CT-1996
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LOCATION: 33..115
OTHER INFORMATION: /codon_start= 33
                                                                                                                   Miettinen-Oinonen, Arja
Londesborough, John
Vehmaanper , Jari
Haakana, Heli
M ntyl , Arja
Lantto, Ralja
Blovainio, Minna
Joutsjoki, Vesa
Paloheimo, Marja
Suominen, Pirkko
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                                          Sequence 30, Application US/09329350 Patent No. 6184019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 936 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: ALKO4237
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20005
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                                                                                                                      APPLICANT:
APPLICANT:
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to: 936

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FEATURE:
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    Sequence 60, Application US/09224681
    Patent No. 620748
    Patent No. 620748
    GENERAL INFORMATION:
    APPLICANT: Esebo, Krisztina M.
    APPLICANT: Suggs, Sidney V.
    APPLICANT: Martin, Robert A.
    APPLICANT: Martin, Rancis H.
    TITLE OF INVENTION: Method for Enhancing the Efficiency of Gene
    TITLE OF INVENTION: Transfer with Stem Cell Factor (SCF), Polypeptide
    NUMBER OF SEQUENCES: 104
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-224-681-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: CUICAGO
STATE: Illinois
COUNTRY: United States of America
ZIP: GOGG-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,681
FILLING DATE:
                                                                                                                                                                                             Percent Identity: 100.000
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APPLICATION DATA:
APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
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APPLICATION NUMBER: 09/005,893
FILING DATE: 12-JAN-1998
CLASSIFICATION:
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FILING DATE: 16-0CT-1989
ATTORNEY, AGENT INFORMATION:
NAME: CLOUGH, DAVIG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/449,653
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US-09-988-687-2 x US-08-482-918-60
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APPLICATION NUMBER: 08/4*
FILING DATE: 24-MAY-1995
CLASSIFICATION:
                                                                                                                   alignment_scores:
Ouality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
mat_peptide
259..1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
NAME/KEY:
                    ; LOCATION:
US-08-482-918-60
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SSEE: Marshall, O'Toole, Gerstein, Murray & Borun
2: 6300 Sears Tower, 233 South Wacker Drive
Chicago
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Percent Identity: 100.000
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APPLICATION NUMBER: US/08/336,728A FILING DATE: 09-NOV-1994 CLASSIFICATION: 424
REFERENCE/DOCKET NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 01017/35199
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 60, Application US/08336728A
Patent No. 6207802
GENERAL INFORMATION:
APPLICANT: Zsebo, Krisztina M.
APPLICANT: Suggs, Sidney V.
APPLICANT: Martin, Francis H.
TTLLE OF INVENTION: Stem Cell Factor
NUMBER OF SEQUENCES: 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicase
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
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APPLICATION NUMBER: 07/982,255
FILING DATE: 25-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/589,701
FILING DATE: 01-0CT-1990
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 07/573,616
FILING DATE: 24-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 AlaAlaGlySerArgAspSerGly 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 GCTGCGGGAAGCAGGGACAGTGGA 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-988-687-2 x US-09-224-681-60
                                                                                                                                                 90:
                                                                                                                                          INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide;
; LOCATION: 259..1002
US-09-224-681-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: 184..1002
                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                        TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 630
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us-09-988-687-2.olip2n.rni

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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-035-706-1
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Ratio: 1.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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; Sequence 1, Application US/09035706
; Patent No. 6001622
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Integrin-Linked Kinase and
; TITLE OF INVENTION: its Uses
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 1404
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastEEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035,706
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/537,198
FILING DATE: 11-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/422,383
FILING DATE: 16-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
REGISTRATION NUMBER: 36,107
RECISTRATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 25-3856
TELEFAX: 25-3856
TELEFX: 25-3856
TELEFX: 25-3856
TELECX: 1404 Dass pairs
LYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPPLOYNEY TELEFAX: 11near
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-336-728A-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-988-687-2 x US-08-336-728A-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 AlaAlaGlySerArgAspSerGly 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: mat_peptide
) LOCATION: 259..1002
US-08-336-728A-60
                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 184..1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-955-841-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
    Sequence 1, Application US/08955841
    Sequence 1, Application US/08955841
    Sequence 1, Application US/08955841
    SENERAL INFORMATION:
    APPLICANT: Dedhar, Shoukat
    APPLICANT: Hannigan, Greg
    TITLE OF INVENTION: Integrin-Linked Kinase and
    TITLE OF INVENTION: 1ts Uses
    NUMBER OF SEQUENCES: 11
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-035-706-1 from: 1 to: 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARRE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/955,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Bozicevic & Reed, LLP
STREET: 285 Hamilton Avenue, Suite 200
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1700 CACTTGCCACATGGTGTCTCCCAA 1723
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: KIN-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 HisLeuProHisGlyValSerGln 230
                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1789 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-035-706-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-988-687-2 x US-09-035-706-1
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REGISTRATION NUMBER: 36,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: KI
TELECOMMUNICATION INFORMATION
TELEPHONE: 650-327-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA
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seq_documentation_block:
    Sequence 1, Application US/07929580B
    Patent No. 2426181
    Patent No. 2426181
    APPLICANT: Lee, Tae Ho
    APPLICANT: Lee, Gene W.
    APPLICANT: Lee, Gene W.
    TITLE OF INVENTION: Cytokine-Induced Protein, TSG-14,
    TITLE OF INVENTION: DNA coding Therefor and Uses Thereof
    NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS:
                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-929-580B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to reverse of: US-07-929-580B-1 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 7355

PRIOR APPLICATION DATA:
APPLICATION UNDRER: 07/640,492
FILING DATE: 14-7AN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, GUY Kevin
REGISTATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: LEE25\VILCEK=2A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,580B
FILING DATE: 19920814
                                                                 to: US-08-669-536-1 from: 1
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US-09-988-687-2 x US-07-929-580B-1/rev
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419 Seventh Street, NW
                                                                                                                              487 GATGCTACACTCTTGATTCATGAG 510
                                                                                                       679 AspAlaThrLeuLeuIleHisGlu 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         624 LeuIleSerSerLeuLeuArgThr 631
    alignment_block:
US-09-988-687-2 x US-08-669-536-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1836 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 8.00
Ratio: 1.000
Percent Similarity: 100.000
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73..606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
US-07-929-580B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GERERAL INFORMATION:
APPLICANT: MASUTA, CHIKARA
APPLICANT: UEHARA, KYOKO
APPLICANT: TANARA, HIDEO
APPLICANT: TANARA, HIDEO
APPLICANT: TOWATA, SHIGERU
TITLE OF INVENTION: ORGANISMS IN WHICH THE EXPRESSION OF
TITLE OF INVENTION: S-ADENOSYLHOMOCYSTEINE HYDROLASE GENE IS INHIBITED
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-669-536-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Gaps: 0
Percent Identity: 100,000
                                                                                                                                                                                   Gaps: 0
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,536
FILING DATE:
                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-955-841-1 from: 1 to: 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ...orkSSEE: BIRCH, STEWART, KOLASCH AND BIRCH STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
    Sequence 1, Application US/08669536
    Patent_No. 5910444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: MORPHY JR, GERALD M
REGISTRATION NUMBER: 28,971
REFRENCE/DOCKET NUMBER: 1254
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                alignment_block:
US-09-988-687-2 x US-08-955-841-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA to mRNA
LENGTH: 1789 base pairs
                                                                                                                                                                                                     Ratio: 1.000
Percent Similarity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
                                                                                                                                                                alignment_scores:
Quality:
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                                                                                                  US-08-955-841-1
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to: 1836

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| AI468143 tf92g05.x1 NCI_CGAP
| AW57577 UT-HF-BMO-ad1-b-07-
| BG227066 602426724F1 NIH_MGC
| BF309436 601892128F1 NIH_MGC
| AW304130 xx13a65.x1 NCI_CGAP
| AA291670 zt37d04.s1 Soares o
| BE386924 601274815F1 NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Olone="Index Septems | Albert | Albert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS BE260495 676 bp mRNA EST 26-OCT-2000
DEFINITION 601150702F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503184 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 ThrGlnHisLeuValLeuAsnGluAsnCysAlaSerValHisAsnLeuAr 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 225
Gaps: 0
Percent Identity: 100.000
       421
493
452
457
404
474
  2.2e-127
2.2e-123
1.9e-122
2.0e-122
1.7e-121
1.9e-120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 676)
NIH-MGC http://mgc.nci.nih.gov/
  140.00 2451.65
136.00 2379.70
135.00 2362.73
135.00 2362.64
134.00 2345.97
133.00 2327.01
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BE260495.1 GI:9131807
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Ratio: 1.000
Percent Similarity: 100.000
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US-09-988-687-2 x BE260495
                                                                                                                                                                                                    seq_name: gb_est1:BE260495
                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
  gb_est1:A1468143
gb_est1:AN75677
gb_est2:B6327066
gb_est1:B7309436
gb_est1:AN304130
gb_est1:AN304130
gb_est1:AB31670
gb_est1:BE386924
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                    About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Unpublished (200)
Contact: Takao Isogai
Genomics Laboratory
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/cell_line="NT2"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells?
Tel: 81-438-52-3951
Exa: 81-438-52-3552
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 213
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                                                                                                                                   Location/Qualifiers
1. 712
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/clone="nn?RM4002610"
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                                                                                                                                                                                                                                                                                                                                             134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 712
                                                                                                                                                                                                                                                                                                                                             204 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 213.00
Ratio: 1.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity: 100.000
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US-09-988-687-2 x AU126037
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human.
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ORGANISM
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KEYWORDS
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                             seq_documentation_block:
LOCUS AU141334 666 bp mRNA EST 25-OCT-2000
DEFINITION AU141334 THYRO1 Homo sapiens cDNA clone THYRO1000421 5', mRNA
                             571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 ysAspProLeuArgHisLeuArgThrArgGluLysArgGlyProSerGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MetTrpAlaLeuCysSerLeuLeuArgSerAlaAlaGlyArgThrMetSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29 ATGTGGGGCGTTTGCTCGCTGCTGCGGTCCGCGGCCGGACGCACTGTC 78
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522 CCACTCTGCCCCAGAATACGAGGATGAAACCATGACAGTTTACCAGATCC
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Gaps: 0
Percent Identity: 100.000
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1153-2: Yana, Kisarazu, Chiba 292-0812, Japan
TTE1: 81-438-55-3951
Fax: 81-438-52-3952
                                                                                                      /tissue_type="thyroid gland"
/note="Vector: pME18SFL3"
186 c 190 g 129 t
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                                                                                                                                                                                                                                                                                      AU141334
AU141334.1 GI:11002855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 666)
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Ratio: 1.000
Percent Similarity: 100.000
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US-09-988-687-2 x AU141334
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VERSION
KEYWORDS
SOURCE
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JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 670) Ota; T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genomics@hri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU143668 670 bp mRNA EST 25-OCT-2000 AU143668 Y79Aa1 Homo sapiens cDNA clone Y79Aa1002297 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 euPheAsnCysGlyGluGlyValGlnArgLeuMetGlnGluHisLysLeu 100
                                                                                                                                                                                                         379 TGTTGGGGGCTTAAGTGGAATGATTCTTACTTTAAAGGAAACCGGGCTTC 428
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                                                                                                                                                                                                                                                                       LysValAlaArgLeuAspAsnIlePheLeuThrArgMetHisTrpSerAs 117
                                                                                                                                                                                                                                                                                                                                                                nValGlyGlyLeuSerGlyMetIleLeuThrLeuLysGluThrGlyLeuP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 IleLysIlePheSerGlyProLeuLysGlyIleGluLeuAlaValArgPr 167
                                                                                      rArgAspSerGlyAlaAlaLeuTyrValPheSerGluPheAsnArgTyrL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OHisSerAlaProGluTyrGluAspGluThrMetThrValTyrGlnIleP
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CysSerGlyGlyProAsnThrValTyrLeuGlnValValAlaAlaGlySe
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Contact: Takkon Isogai
Connics: Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Fax: 81-438-52-3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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AU143668
AU143668.1 GI:11005189
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LOCUS AU143668
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HRI human
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us-09-988-687-2.olip2n.rst

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ccesacrcssccccsccrcracercrrccsacrcaaccssrarc 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 roLysCysValLeuSerGlyProProGlnLeuGluLysTyrLeuGluAla 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
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                                                                                  others
                                                                                                                                                                                                                                                   1 MetTrpAlaLeuCysSerLeuLeuArgSerAlaAlaGlyArgThrMetSe 17
                                                                                                                                                                                                                                                                                                 17 rGlnGlyArgThrIleSerGlnAlaProAlaArgArgGluArgProArgL 34
                                                                                                                                                                                                                                                                                                                                                                                             CysSerGlyGlyProAsnThrValTyrLeuGlnValValAlaAlaGlySe
                                                                                                                                          Length: 203
Gaps: 0
Percent Identity: 100.000
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193 g 127
                                                                                                                                                                                                                            Align seg 1/1 to: AU143668 from: 1 to: 670
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                                                                               190 c
                                                                                                                                          Quality: 203.00
Ratio: 1.000
Percent Similarity: 100.000
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US-09-988-687-2 x AU143668
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                                                                                                                                alignment_scores
                                                                                BASE COUNT
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/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
/note: lorgan: adrenal gland; Vector: pCMV-SPORT6 for primed. Average insert size 1.229 kb. Library enriched for full-length clones and constructed by Life Technologies.
/note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                 Homo sapiens Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Makaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 944)
1 (hases 1 trp://mgc.ncl.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            þe
                                         seq_documentation_block:
LOCUS BF969043 944 bp mRNA EST 22-JAN-2001
DEFINITION 602269966F1 NIH_MGC_84 Homo sapiens CDNA clone IMAGE:4357985
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lattribution information can lattribution; MGC E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9995 row: d column: 18
High quality sequence stop: 591.
Location/Qualifiers
1. 944
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                             BF969043.1 GI:12336258
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Percent Similarity: 100.000
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Ratio: 1.000
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seq_name: gb_est2:BF969043
                                                                                                                    mRNA sequence.
BF969043
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ORIGIN
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AUTHORS
TITLE
JOURNAL
                                                                                                                                          ACCESSION
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SOURCE
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601298656F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3629028 5

BE382353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 ThrGlnHisLeuValLeuAsnGluAsnCysAlaSerValHisAsnLeuAr
                                                                                                                                                                                                                                                                                             1 ACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACATCACTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProMetValGlnGlyGluCysLeuLeuLysTyrGlnLeuArgProArgAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 CCCATGGTTCAGGGTGAATGCCTCCTCAAGTACCAGCTCCGTCCCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 GGAGTGGCAGAGGGATGCCATTATTACTTGCAATCCTGAGGAATTCATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 GACTGTGGTGAGGGCACATTTGGGCAGCTGTGCCGTCATTACGGAGACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alGluAlaLeuGlnLeuProAsnPheGlnGlnSerValGlnGluTyrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AspCysGlyGluGlyThrPheGlyGlnLeuCysArgHisTyrGlyAspGl
                                                                                                                                                                                                                                                                                                                                                                                                                                   roLeuLeuThrSerPheArgCysLysLysGluGlyProThrLeuSerVal
                                                                                                                     Gaps: 0
Percent Identity: 100.000
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137
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    O
                                                                                             Quality: 197.00
Ratio: 1.000
Percent Similarity: 100.000
  199
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LOCUS BE382353
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  154
                                                                                                                                                                          alignment_block:
US-09-988-687-2 x
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KEYWORDS
SOURCE
ORGANISM
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                  ORIGIN
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Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 664)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs remail nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM313 row: a column: 13
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A EST 21-JUL-2000 sapiens cDNA clone IMAGE:3628308
                                                                                                           415
201 GGCAGATGCCCCCGTGGCCTTGGTGGTTCACATGGCCCCCAGCATCTGTGC 250
                                                                                                                                                                                          382 rHisLysIleGlnThrGlnLeuAsnLeuIleHisProAspIlePheProL 399
                                                                                                                                                                                                            416 MetValGlnGlyGluCysLeuLeuLysTyrGlnLeuArgProArgArgGl 432
                                                                                                                                                                                                                                                                                                                                                                        432 uTrpGlnArgAspAlaIleIleThrCysAsnProGluGluPheIleValG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                     449 luAlaLeuGlnLeuProAsnPheGlnGlnSerValGlnGluTyrArg 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 euLeuThrSerPheArgCysLysLysGluGlyProThrLeuSerValPro
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Location/Qualifiers
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BE383336
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SOURCE
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erSerLeuLeuArgThrCysAspLeuGluGluPheGlnThrCysLeuVal

626

609 sLeuGlnGluGlyAlaGluIleSerSerProAlaValGluArgLeuIleS

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alignment_block:
US-09-988-687-2 x BF797306
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//lab.host="hHIOB (phage-resistant)"
//nab.host="nHIOB (phage-resistant)"
//nab.host="nHIOB (phage-resistant)"
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//nab.host="nho" priming sites using the following 5'
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//nab.host="nho" priming ZAP-CDNA synthesis kit
//stratagene) and Superscript II RT (Life Technologies).
//nab.host="nho" priming ZAP-CDNA synthesis kit
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 692) NIH-WGC http://mgc.nci.nih.gov/. NIH-WGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (WGC)
                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 600.
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/clone="IMAGE:3629028"
                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_19"
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Percent Similarity: 100.000
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US-09-988-687-2 x BE382353
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Ratio:
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JOURNAL
                                                                                         REFERENCE
AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 960)

1 (Dases 1 to 960)

2 NIH-MGC http://mgc.ncl.nih.gov/.

3 NIH-MGC http://mgc.ncl.nih.gov/.

3 Dubbished (1999)

3 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-remail.nih.gov

7 Tissue Procurement: Louis Staudt, M.D., Ph.D.

5 CDNA Library Preparation: Life Technologies, Inc.

6 CLONG distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

6 http://image.llh.gov

7 Column: 07

8 High quality sequence stop: 705.

10 Location/Qualifiers
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Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                      602256926F1 NIH_MGC_85 Homo sapiens CDNA clone IMAGE:4340286 5', BF797306
                   452
                                                                     629
                                                                                                                    502
                                                                  Gaps: 0
Percent Identity: 100.000
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Quality: 194.00
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LOCUS BF797306
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ThrGlnLeuAsnLeuIleHisProAspIlePheProLeuLeuThrSerPh
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0.936
99.510
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG396395 827 bp mRNA EST 12-MAR-2001 602459323F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4581700 5 mRNA sequence.
BG396395 GI:13289941
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                                                                                                           488
                                                                                                                          52 AGCCCCAGCAGAAAAAAAAAGTCAGTACCCAGAAAATCATCTTGGAA 101
                                                                                                                                                                                                     102 CAGGGTCTGCCCATCCCGATGAAGATTCGAAATGTCAGTGCCACACTTGTC 151
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                                                                                                                                                                                                                                                                              152 AACATAAGCCCCGACACGTCTCTGCTACTGGACTGTGGGGGGACGTT 201
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                                                                       51
                                455 AsnPheGlnGlnSerValGlnGluTyrArgArgSerAlaGlnAspGlyPr
                                                                     2 AACTICCAGCAGAGCGTGCAGGAGTACAGGAGGAGGACGGCCC
                                                                                                                                                                                                                                                                                                                                                   502 GGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATCTGGAAGAGTTTC
                                                                                                         471 oAlaProAlaGluLysArgSerGlnTyrProGluIleIlePheLeuGlyT
                                                                                                                                                                                  488 hrGlySerAlaIleProMetLysIleArgAsnValSerAlaThrLeuVal
                                                                                                                                                                                                                                                           505 AsnIleSerProAspThrSerLeuLeuLeuAspCysGlyGluGlyThrPh
                                                                                                                                                                                                                                                                                                                                    eGlyGlnLeuCysArgHisTyrGlyAspGlnValAspArgValLeuGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            352 GCCGCTTCACCCTTTGCTGGTGGTTGCCCCCAACCAGCTCAAAGCCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       605 IleProAlaLysCysLeuGlnGluGlyAlaGluIleSerSerProAlaVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 ATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              621 lGluArgLeuIleSerSerLeuLeuArgThrCysAspLeuGluGluPheG
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 from: 1
to: BF797306
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LOCUS BG396395
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KEYWORDS
SOURCE
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/clone="INAGE.4581700"
/clone="INAGE.4581700"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: Grown: eye; Vector: pOTB7; Site_1: XhoI; Site_2: CorsI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM1302 row: n column: 05
High quality sequence stop: 779.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424 TGAATGAGAACTGTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 99.510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 827
                                                                                                                                                 /organism="Homo sapiens'/db_xref="taxon:9606"
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MetTrpAlaLeuCysSerLeuLeuArgSerAlaAlaGlyArgThrMetSe
                                          36 ATGTGGGCGCTTTGCTCGCTGCGGTCCGCGGCCGGACGCACCATGTC
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshhyuki and Piero Carninot (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLAM10753 row: g column: 12

High quality sequence stop: 728.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                    BG719016 735 bp mRNA EST 08-MAY-2001 602699144F1 NIH_MGC_97 Homo sapiens CDNA clone IMAGE:4831139
                                                                                                                            474 ACCCAGCTCAACCTCATCCACCGGACATCTTCCCCCTGCTCACCAGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BG719016
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LOCUS
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Ratio:
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to: 735

from: 1

to: BG719016

Align seg 1/1

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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6024555471 NIH_MGC_15 Home sapiens CDNA clone IMAGE:4583679 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 920)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
185
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                                                                                                                                                                                                                                                                                                                                             336 AAGGTTGCTCGCCTGGACAACATATTCCTGACACGAATGCACTGGTCTAA 385
                                                                                                                                                                                                                                                                                                                                                                         134
                                                              20
                                                                                                                         29
                                                                                                                                                                                    84
                                                                                                                      67 rArgAspSerGlyAlaAlaLeuTyrValPheSerGluPheAsnArgTyrL
                                                                                                                                                                                                                   236 CCGGGACTCGGGCGCCGCGCTCTACGTCTTCTCCGAGTTCAACCGGTATC
                                                                                                                                                                                                                                                                                                                                                                                         151 IleLysIlePheSerGlyProLeu.LysGlyIleGluLeuAlaValArgP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysValAlaArgLeuAspAsnIlePheLeuThrArgMetHisTrpSerAs
                                                                                                                                                                                                                                                                                                                                                                         117 nValGlyGlyLeuSerGlyMetIleLeuThrLeuLysGluThrGlyLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                        roLysCysValLeuSerGlyProProGlnLeuGluLysTyrLeuGluAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 ATCAAAATTTTCTGGTCCATTGAAAAGGAATAGAACTGGCTGTGCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roHisSerAlaProGluTyrGluAspGluThrMetThrValTyrGlnIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BG386090
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306 PheValValValGluCysProAspGluSerPheIleGlnProIleCysGl 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 euValValHisMetAlaProAlaSerValLeuValAspSerArgTyrGln 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlnTrpMetGluArgPheGlyProAspThrGlnHisLeuValLeuAsnG1 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 uAsnCysAlaSerValHisAsnLeuArgSerHisLysIleGlnThrGlnL 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 GAACTGTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTCAAACCCAGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     euAsnLeuIleHisProAspIlePheProLeuLeuThrSerPheArgCys 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysLysGluGlyProThrLeuSerValProMetValGlnGlyGluCysLe 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            422 uLeuLysTyrGlnLeuArgProArgArgGluTrpGlnArgAspAlaIleI 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        439 leThrCysAsnProGluGluPheIleValGluAlaLeuGlnLeuProAsn 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                                                                                                                                                                                                           21 TTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCATTCAACCCATCGTGA
                                                                                                                                                                                                                                                                                                              Length: 186
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 920
                                                                                                                                                                                                                                                                                                                        Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: BG386090
                                                                                                                                                                                                                                                                                                                                                          alignment_block:
us-09-988-687-2 x BG386090
                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                           source
                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406
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                                                                               FEATURES
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/tissue_type="adenocarcinoma cell line"
/tasue_type="adenocarcinoma cell line"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1012)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS BG386348 1012 bp mRNA EST 12-MAR-2001
DEFINITION 60245550F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4583749 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM1308 row: c column: 14
High quality sequence stop: 675.
                                                                                                                                                     300 ProAspProGlyAlaAlaPheValValValGluCysProAspGluSerPh 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 199
Gaps: 1
Percent Identity: 99.497
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BG386348
BG386348.1 GI:13279794
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0.934
99.497
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US-09-988-687-2 x BG386348
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                                                                                                                                                                                                                                                                                                                489 lySerAla 491
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VERSION
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JOURNAL
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AUTHORS
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High quality sequence stop: 507
Location/Qualifiers
primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 184.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-988-687-2 x BF434169
                                                                                                                                                                                                                                                                                                                                                                                          143
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                                                                 source
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento
Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 553)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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LOCUS BR434169 553 bp mRNA EST 29-NOV-2000
DEFINITION 7099f04.x1 NCI_CGAP_OV18 Homo sapiens cDNA clone IMAGE:3644670
similar to TR:Q9V5J4 Q9V5J4 CG3298 PROTEIN. ;, mRNA sequence.
ACCESSION BF434169
                                                                                                                                                                                                                                                                                                                                                                                          303
                                                                                                                                                                                                                                                                                                                                                                                                                              elleGlnProlleCysGluAsnAlaThrPheGlnArgTyrGlnGlyLysA 333
                                                                                                                                                                                350 ValaspSerargTyrGlnGlnTrpMetGluArgPheGlyProAspThrGl 366
                                                                                                                                                                                                                                                              HisLysIleGlnThrGlnLeuAsnLeuIleHisProAspIlePheProLe 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TrpGlnArgAspAlaIleIleThrCysAsnProGluGluPheIleValGl 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              etValGlnGlyGluCysLeuLeuLysTyrGlnLeuArgProArgArgGlu 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uAlaLeuGlnLeuProAsnPheGlnGlnSerValGlnGluTyrArgArgS 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               erAlaGlnAspGlyProAlaProAlaGluLysArgSerGlnTyrProGlu 482
                                                                                                                       104 CAGATGCCCCCGTGGCCTTGGTGTTCACATGGCCCCAGCATCTGTGCTT
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                                                                                                                                                                                                                                                                                                                                                                                        CACAAGATTCAAACCCAGCTCAACCTCATCCACCGGACATCTTCCCCCT
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TITLE
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KEYWORDS
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                     316
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SOURCE

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400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151 AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGA 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 ACTGGTCTAATGTTGGGGGCTTAAGTGGAATGATTCTTACTTTAAAGGAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 laValArgProHisSerAlaProGluTyrGluAspGluThrMetThrVal 180
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                                                                                                                                                                                                                                                                                                                                                                           64
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                                                                                                                                                                                                                                                                                                                                           1 | CGCCGCGCAAGGACCCGCTGCGCACCTGCGCACGCGAGAAGCGCGG
                                                                                                                                                                                                                                                                                                                                                                           47 yProSerGlyCysSerGlyGlyProAsnThrValTyrLeuGlnValValA
                                                                                                                                                                                                                                                                                                                                                                                      AsnArgTyrLeuPheAsnCysGlyGluGlyValGlnArgLeuMetGlnGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 ThrGlyLeuProLysCysValLeuSerGlyProProGlnLeuGluLysTy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 rLeuGluAlaIleLysIlePheSerGlyProLeuLysGlyIleGluLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 ArgProArgLysAspProLeuArgHisLeuArgThrArgGluLysArgGl
                                                                                                                                                                                                                               Length: 184
Gaps: 0
Percent Identity: 100.000
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588

772

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522 lyGlnLeuCysArgHisTyrGlyAspGlnValAspArgValLeuGlyThr 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         673 CGCTTCACCCTTTGCTGGTGGTTGCCCCCAACCAGCTCAAAGCCTGGCTC 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnGlnTyrHisAsnGlnCysGlnGluValLeuHisHisIle.SerMetI 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 GlySerAlaIleProMetLysIleArgAsnValSerAlaThrLeuValAs
                                                                                                                                                                                                                                                                   nlleSerProAspThrSerLeuLeuAspCysGlyGluGlyThrPheG
                                                                                                                                                                                                                                                                                                     605 leProAlaLysCysLeuGlnGluGlyAlaGluIleSerSerProAlaVal
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   472 laProAlaGluLysArgSerGlnTyrProGluIleIlePheLeuGlyThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               823 GAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAA 864
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LOCUS BG756043
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Listue_Type="neuroblastoma"
//Listue_Type="neuroblastoma"
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//Lab_host="neur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 884)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: ArCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM176 row: d column: 01
High quality sequence stop: 859.
Location/cualifiers
1. 884
                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS BG519751 884 bp mRNA EST 02-APR-2001
DEFINITION 602578902F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3503184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pGlnSerProGluArgProLeuSerArgLeuSerProGluArgSerSerA 214
                              439 IleThrCysAsnProGluGluPheIleValGluAlaLeuGlnLeuProAs 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 ATTACTTGCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           455 nPheGlnGlnSerValGlnGluTyrArgArgSerAlaGlnAspGlyProA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaps: 1
Percent Identity: 99.495
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/db_xref="taxon:9606"
/clone="IMAGE:3503184"
/clone_lib="NIH_MGC_19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG519751.1 GI:13515513
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US-09-988-687-2 x BG519751
                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BG519751
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KEYWORDS
SOURCE
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197
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
602716533F1 NJH_MGC_48 Homo sapiens CDNA clone IMAGE:4856360 5', mRNA sequence.
BG756043 GI:14066696
                                                                                                                                                                                                                                                                                                                                                                                                                        Mactorias in the contact: Nobert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI707 row: b_column: 09
                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 890)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
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/issue_type="primary B-cells from tonsils (cell line)"
/iab_host="Drimary B-cells from tonsils (cell line)"
/iab_host="DH100 (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhOI;
Site_2: BacNY: cDNA made by oligo-dT priming.
Directionally cloned into EcoRIX/XhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                erGlnArgTyrAlaLysValProLeuPheSerProAsnPheSerGluLys 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302 GTGGGAGTTGCCTTTGACCACATGAAGGTCTGCTTTGGAGACTTTCCAAC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 luGluMetGluGluArgArgGluLysArgGluLeuArgGlnValArgAla 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 TGGGGAAAGATGCCACCCTCCTGATACATGAAGCCACCCTGGAAGATGGT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 TTGGAAGAGGAAGCAGTGGAAAAGACACACACCACAACGTCCCAAGCCAT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 GCCAGCGCTATGCCAAGGTCCCCCTTTCAGCCCCAACTTCAGCGAGAAA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             743 ValGlyValAlaPheAspHisMetLysValCysPheGlyAspPheProTh 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       759 rMetProLysLeuIleProProLeuLysAlaLeuPheAlaGlyAspIleG 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         693 LeuGluGluGluAlaValGluLySThrHisSerThrThrSerGlnAlail
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            643 ArgHisCysLysHisAlaPheGlyCysAlaLeuValHisThrSerGlyTr
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 100.000
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Ratio: 1.000
Percent Similarity: 100.000
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US-09-988-687-2 x BG756043
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552 AG 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
111.95
111.95
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111.72
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 88.00
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Gaps: 0
Percent Identity: 100.000
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51..2531
/*tag= a
/product= "HPC2"
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Percent Similarity: 100.000
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P-PSDB; AAB07228.
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8.1e-06
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Database sequences: 930621
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of: US-09-988-687-2
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567 1751	aSerLeuGlyLysProLeuHisProLeuLeuValValAlaProAsnGlnL 	584 1800
58 4 1801	euLysAlaTrpLeuGlnGlnTyrHisAsnGlnCysGlnGluValLeuHis 	1850
601	HisileSerMetileProAlaLysCysLeuGlnGluGlyAlaGlulleSe 	617 1900

us-09-988-687-2.olip2n.rng

634

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                                                                                                                          P-PSDB; AAY99850
                                                                                                                                                                                                                                                                                                  patient's genome
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Quality:
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                                          09-DEC-1999;
                         15-JUN-2000
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Human sulphatase G; hSG; chromosome 17p11.2; gene therapy; ss
                2350
                                                                                                                                                                                                                                                                                                                                  2451 GCCGCCTGGAGGATGGGGAGCCTCAGCAGAAGCGGGCCCACACAGAGGA 2500
                                                                             667
                                                                                                                                                                                       717
                                                                                                                                                                                                                         717 aGluPheIleMetLeuAsnHisPheSerGlnArgTyrAlaLysValProL 734
                                                                                                                                                                                                                                                              euPheSerProAsnPheSerGluLysValGlyValAlaPheAspHisMet 750
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                                         euGluGluPheGlnThrCysLeuValArgHisCysLysHisAlaPheGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2528
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1..2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2501 GCCACAGGCCAAGAAGGTCAGAGCCCAG
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/product= "hSG"
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ID AAA52810 standard; cDNA; 2478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human sulphatase G cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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801

Key

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not a member of the well-characterised CTPSR sulphatase family.

It belongs to a family showing sequence similarity to a sulphatase from the marine bacterium Alteromonas carrageenovora. The hSG gene contains 23 exons and is located at chromosome 17pll.2. The present sequence is clone lambda29.1 from a human testes cDNA library. It was isolated using human EST sequences with sequence similarity to the non-CTPSR family as a probe to screen the library. The cDNA insert was subcloned and the DNA sequence of both strands was determined. The sequence may be used to treat a patient suffering from hSG deficiency by replacing, repairing, or compensating for a DNA sequence within that
                                                                                                                                                                                                                                                   Novel isolated DNA sequence which encodes human sulfatase G or its fragment useful in gene therapy for treating patients suffering from sulfatase deficiency -
                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes human sulphatase G (hSG). hSG is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCTCCGGCGCCCAAACACCGTGTACCTGCAGGTGGTGGCAGCGGGTAG 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysSerGlyGlyProAsnThrValTyrLeuGlnValValAlaAlaGlySe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rArqAspSerGlyAlaAlaLeuTyrValPheSerGluPheAsnArgTyrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 99.758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2478 BP; 587 A; 686 C; 709 G; 496 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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                                                                                         (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 29-30; 33pp; English
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99WO-AU01092
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584	euLysAlaTrpLeuGlnGlnTyrHisAsnGlnCysGlnGluValLeuHis 	1800
601	His II eserMet II eProAlaLysCysLeuGlnGluGlyAlaGluI lese 	617 1850
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651	CysAlaLeuValHisThrSerGlyTrpLysValValTyrSerGlyAspTh 	667 2000
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684 2051	leHisGluAlaThrLeuGluAspGlyLeuGluGluGluAlaValGluLys 	700
701	Thrhisserthrthrserglnalaileservalglymetargmetasnal 	717 2150

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P-PSDB; AAB42236.
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 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosupressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antidibetical; antidiabetic; antidibetical; sardicovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
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                                                                                                                                                                                                                                                                                                                     817
               717 aGluPheIleMetLeuAsnHisPheSerGlnArgTyrAlaLysValProL 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ORFX ORF2000 polynucleotide sequence SEQ ID NO:3999
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                                                                                                                                                                                                                                                                                                                                                                                817 uProGlnAlaLysLysValArgAlaGln 826
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ID AAC76445 standard; cDNA; 2546 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   thrombosis; contraceptive; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-602362/57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC76445;
                                                                         734
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which represent the human ORRX oper reading frames 1 to 3161. The ORRX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetlc; hypotensive; dermatological; immunosuppressive; antidiabetlc; hypotensive; dermatological; immunosuppressive; antidiabetlc; hypotensive; dermatological; antidiabetlc; hypotensive; dermatological; antidiabetlc; predisposition to, or preventing or treating pathological conditions associated with an OREX associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus bacterial or fungal infection, malaria, autoimmune disorders, asthma, cortering and infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                                      AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sGluAsnAlaThrPheGlnArgTyrGlnGlyLysAlaAspAlaProValA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661 CAGCAGTGGATGGAGGTTTGGCCTGACACCCAGCACTTGGTCCTGAA 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlnGlnTrpMetGluArgPheGlyProAspThrGlnHisLeuValLeuAs 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2546 BP; 652 A; 643 C; 686 G; 564 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 eAlaProlleIleAlaAlaValLysAspGlyLysSerIleThrHisGluG
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Percent Identity: 99.825
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                                                                                                                                              Claim 5; Page 3179-3180; 5507pp; English
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99.825
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hrLeuGluAspGlyLeuGluGluGluAlaValGluLysThrHisSerThr

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160	404	421	438	454	471 1010	488 1060	50 4 1110	521 1160	538 1210	554 1260	571 1310	588 1360	604 1410	621 1460	638 1510	654 1560	671 1610	688 1660
TGAGAACTGTGCCTCAGTTCACAACCTTCGCAGCCACAAGATTCAAACCC	InteuasnieulleHisProaspilePheproLeuleuThrSerPhearg 	CysLysLysGluGlyProThrLeuSerValProMetValGlnGlyGluCy 	SLeuLeulysTyrGlnLeuArgProArgArgGluTrpGlnArgAspAlal	ellethrcysasnProGluGluPhelleValGluAlaLeuGlnLeuDro	AsnPheGlnGlnSerValGlnGluTyrargArgSerAlaGlnAspGlyPr 	oAlaProAlaGluLysArgSerGluTyrProGluIleIlePheLeuGlyT 	hrdlyseralaileprometlysileargasnvälseralaihrLeuval 	AsnIleSerProAspThrSerLeuLeuLeuAspCysGlyGluGlyThrPh 	eGlyGlnLeuCysArgHisTyrGlyAspGlnValAspArgValLeuGlyT 	hrLeualaalavalphevalSerHisLeuHisAlaaspHisHisThrGly 	LeuproserileLeuleuGinargGluargAlaLeuAlaserLeuGlyLy 	SProLeuHisProLeuLeuValValAlaProAsnGlnLeuLysAlaTrpL 	euGlnGlnfyrHisAsnGlnCysGlnGluValLeuHisHisTleSerWet 	IleproAlaLysCysLeuGlnGluGlyAlaGluIleSerSerProAlaVa 	GluargLeulleSerSerLeuLeuargThrCysaspLeuGluGluPheG 	InthrCysLeuValArgHisCysLysHisAlaPheGlyCysAlaLeuVal 	HisThrSerGlyTrpLysValValTyrSerGlyAspThrMetProCysGl	ualaLeuValargMetGlyLysaspalaThrLeuLeuIleHisGlualaT
711	388 761	405	421 861	438	455 961	471 1011	488	505	521 1161	538 1211	555 1261	571 1311	588 1361	605	621 1461	638 1511	655 1561	671 1611

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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito K, Yamamoto J;
Otsuki T;
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1810
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                                                                                                                                                                                               ThrSerGlnAlalleSerValGlyMetArgMetAsnAlaGluPheIleMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 heAlaGlyAspIleGluGluMetGluGluArgArgGluLysArgGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        788 ArgGlnValArgAlaAlaLeuLeuSerArgGluLeuAlaGlyGlyLeuGl
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A, Nagai K,
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Sugiyama T, Wakamatsu
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ID AAH14250 standard; cDNA; 2976
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary trand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the polynucleotide which comprises a 3'-end sequence, where the polynucleotide which comprises a 1'-end sequence, where the polynucleotide comprises at least 15 nucleotides and the combination of the Stend sequence/37 end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13613 to AAH13628 and AAH13633 to AAH13632 to AAH13639 to AAH13632 to AAH13632 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification and/or diagnosis of the abnormality of the proteins encoded by English SEQ ID 11557; 2537pp + CD ROM; the present invention. full-length cDNAs Claim 8;

Sequence 2976 BP; 712 A; 807 C; 856 G; 601 T; 0 other;

Percent Identity: 99.602 Length: Gaps: 0.573 430.00 US-09-988-687-2 x AAH14250 Quality: Percent Similarity: Ratio: alignment_scores alignment_block:

from: 1 Align seg 1/1 to: AAH14250

1 MetTrpAlaLeuCysSerLeuLeuArgSerAlaAlaGlyArgThrMetSe 17

20 34 ysaspProLeuArgHisLeuArgThrArgGluLysArgGlyProSerGly

67 51 CysSerGlyGlyProAsnThrValTyrLeuGlnValValAlaAlaGlySe

84 67 rArgAspSerGlyAlaAlaLeuTyrValPheSerGluPheAsnArgTyrL

84 euPheAsnCysGlyGluGlyValGlnArgLeuMetGlnGluHisLysLeu 100 101 LysValAlaArgLeuAspAsnIlePheLeuThrArgMetHisTrpSerAs 117

425 TGTTGGGGGCTTAAGTGGAATGATCTTACTTTAAAGGAAACCGGGCTTC 474 nValGlyGlyLeuSerGlyMetIleLeuThrLeuLysGluThrGlyLeuP 134

1074 1125 GACAGCAGGTACCAGCAGTGGATGGAGGTTTGGGCCTGACACCCCAGCA 1174 1175 CTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTTCGCAGCCACA 1224 1225 AGATTCAAACCCAGCTCAACCTCATCCACCGGACATCTTCCCCCTGCTC 1274 417 200 250 300 317 367 384 217 267 874 434 InArgAspAlaIleIleThrCysAsnProGluGluPheIleValGluAla 450 524 167 184 674 724 234 GAATGAAAATGAGCCACACCTTCCACATGGTGTTAGCCAGAGAAGAGGGG 774 925 TCACTCATGAAGGAAGAGATTTTGGCTGATGAAGAGCTGTGTACTCCTCCA 975 GATCCTGGTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCAT 317 eGlnProIleCysGluAsnAlaThrPheGlnArgTyrGlnGlyLysAlaA 1025 TCAACCCATCTGTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAG 1275 ACCAGTTTCCGCTGT...AAGGAGGCCCCACCCTCAGTGTGCCCATGGT OHisSerAlaProGluTyrGluAspGluThrMetThrValTyrGlnIleP alArgAspSerSerLeuValValAlaPheIleCysLySLeuHisLeuLys 775 TCAGGGACTCTTCCCTGGTCGTAGCTTTCATCTGTAAGCTTCACTTAAAG 825 AGAGGAAACTICTIGGIGCICAAAGCAAAGGAGAIGGGCCICCCAGIIGG yThrAlaAlaIleAlaProIleIleAlaAlaValLysAspGlyLysSerI 284 leThrHisGluGlyArgGluIleLeuAlaGluGluLeuCysThrProPro 301 AspProGlyAlaAlaPheValValValGluCysProAspGluSerPheIl AspSerArgTyrGlnGlnTrpMetGluArgPheGlyProAspThrGlnHi sLeuValLeuAsnGluAsnCysAlaSerValHisAsnLeuArgSerHisL 384 ysileGlnThrGlnLeuAsnLeuIleHisProAspIlePheProLeuLeu 401 ThrSerPheArgCysLysLysLysGluGlyProThrLeuSerValProMetVa 417 IGInGlyGluCysLeuLeuLysTyrGlnLeuArgProArgArgGluTrpG roLysCysValLeuSerGlyProProGlnLeuGluLysTyrLeuGluAla 151 IleLysIlePheSerGlyProLeuLysGlyIleGluLeuAlaValArgPr ATCAAAATATTTTCTGGTCCATTGAAAGGAATAGAACTGGCTATGCGGCC rAsnGluAsnGluProHisLeuProHisGlyValSerGlnArgArgGlyV ArqGlyAsnPheLeuValLeuLysAlaLysGluMetGlyLeuProValGl 725 351 134 167 575 184 625 201 675 217 234 875 367 251 267

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1372 AGAGGGATGCCATTATACTTGCAATCCTGAGGAATTCATAGTTGAGGCG 1421
                                                                                                                1422 CIGCAGCTICCCAACTICCAGCAGAGCGIGCAGGAGTACAGGAGGAGIGC 1471
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                                                                                                                                                              467 aGlnAspGlyProAlaProAlaGluLysArgSerGlnTyrProGluIleI
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                                                                                                                                                                                                                                                                                                                                                       AlaThrLeuValAsnIleSerProAspThrSerLeuLeuAspCysGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617 rSerProAlaValGluArgLeuIleSerSerLeuLeuArgThrCysAspL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euGluGluPheGlnThrCysLeuValArgHisCysLysHisAlaPheGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2022 TGTGCGCTGCTGCACACCTCTGGCTGGAAAGTGGTCTATTCCGGGGACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                684 leHisGluAlaThrLeuGluAspGlyLeuGluGluGluAlaValGluLys
                                                                      LeuGlnLeuProAsnPheGlnGlnGlnSerValGlnGluTyrArgArgSerAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        601 HisIleSerMetIleProAlaLysCysLeuGlnGluGlyAlaGluIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rMetProCysGluAlaLeuValArgMetGlyLysAspAlaThrLeuLeuI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701 ThrHisSerThrThrSerGlnAlaIleSerValGlyMetArgMetAsnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aGluPheIleMetLeuAsnHisPheSerGlnArgTyrAlaLysValProL
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detection; diagnosis; antisense therapy; gene therapy; ss.
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2272 TCTTCAGCCCCAACTTCAGCGAGAAGTGGGAGTTGCCTTTGACCACATG 2321
                                              seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH05835
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Wakamatsu A, Nagai K, Otsuki T;
                                                                                                                    Human cDNA clone (5'-primer) SEQ ID NO:2670.
                                                                      BP
                                                                                                                                                                                                                                                                            Isogai T, Nishikawa T,
                                                                     AAH05835 standard; cDNA; 584
                                                                                                                                                                                                                     99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                              99JP-0248036
                                                                                                                                                                                                                                               2000JP-0241899
                                                                                                    (first entry)
                                                                                                                                                                                                                                                             (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                     Sugiyama T,
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                                                             seq_documentation_block:
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               751 LysvalCys 753
                                                                                                                                   Human; primer;
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                             09-JUN-2000;
                                                                                                                                                   Homo sapiens
                                                                                                                                                                 EP1074617-A2
                                                                                                                                                                                                              29-JUL-1999;
                                                                                                    26-JUN-2001
                                                                                                                                                                                 07-FEB-2001
                                                                                                                                                                                                                                                                           Ota T, Is
Ishii S,
                                                                                    AAH05835;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptrises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a jugonucleotide comprises a 3'-end sequence. The primer sets and sequence complementary to a polynucleotide which comprises a 3'-end sequence. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers are also useful for AMH1318 and complementary in the full-length cDNAs. The primers are also useful for AMH1318 and complementary in the full-length cDNAs. The primers allow obtaining of the full-length cDNAs assily without any specialised methods. AMH03166 to AMH1318 and AMH18742 represent human cDNA sequences. AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification the present invention.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the

Claim 1; SEQ ID 2670; 2537pp + CD ROM; English.

full-length cDNAs

Sequence 584 BP; 122 A; 166 C; 178 G; 115 T; 3 other

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Human; prostate cancer predisposing gene; HPC2; chromosome 17p;
gene therapy; peptide therapy; drug design; ds.
                                                                                                                                                                                                                                                                                                                                                                    Human prostate cancer predisposing gene HPC2 genomic sequence.
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Ratio: 1.000
Percent Similarity: 100.000
                                 alignment_block:
US-09-988-687-2 x AAH05835
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                                                                                                                                                                                                                                                                                                                                       AAA60207;
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W09964576-A2
AXB
                                                                                                                                                                                                                                             The present sequence is the genomic sequence of the human prostate cancer predisposing gene HPC2, which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs. This sequence was isolated by cloning and sequencing the region of the genome which appeared to cause a predisposition to prostate cancer.
                                                                                                                                                 Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene expression product; diagnosis; tumour; colon cancer; colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 26664 BP; 6173 A; 6300 C; 6519 G; 7661 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human colon cancer cell line SW480 cDNA clone SEQ ID NO:315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1010 AGGACCCGTGCGCCACCTGCGCACGAGAAGCGCGGACCGTCGGGG 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 ysAspProLeuArgHisLeuArgThrArgGluLysArgGlyProSerGly 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetTrpAlaLeuCysSerLeuLeuArgSerAlaAlaGlyArgThrMetSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 rGlnGlyArgThrIleSerGlnAlaProAlaArgArgGluArgProArgL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 CysSerGlyGlyProAsnThrValTyrLeuGlnValValAlaAlaGlySe 67
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Gaps: 0
Percent Identity: 100.000
                                                       Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 26664
                                                                                                                                                                                                           Claim 3; Page 108-122; 157pp; English.
                                                     Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAA60207 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ80231 standard; cDNA; 238 BP
               (MYRI-) MYRIAD GENETICS INC.
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                                                     Teng DHF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouality: 82.00
Ratio: 1.000
Percent Similarity: 100.000
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                                                     Pavtigian SV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The colon connes can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia,
                                                                                                                                                                                                                                                                                                      Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer
                                                                                                                                                                               Monahan JE;
                                                                                                                                                    Bushnell SE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 rgLeuMetGlnGluHisLysLeuLysValAlaArgLeuAspAsnIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 CTGACACGAATGCACTGGTCTAATGTTGGGGGGCTTAAGTGGAATGATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 uThrLeuLysGluThrGlyLeuProLysCysVal 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 TACTITAAAGGAAACCGGGCTTCCAAAGTGTGTA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 238
                                                                                                                                                          Astle JH,
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 258; 469pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 238 BP; 55 A; 57 C; 69 G;
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                                                  98US-0088801
                                                                                                                                                          Steinmann KE,
Catino TJ, De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dysplasia or hyperplasia.
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1.000
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09-JUN-1999;
                                                  10-JUN-1998;
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                                                                                                                                                                                                       Schlegel R;
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0135124
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                                                                                                                                                                                                        99US-0128234
                                                                                                                                                                                                                            99US-0129845
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                                                                                                                                                                                                                                                                     99US-0130891
                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-013
                                           Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
25-MAY-1999;
25-MAY-1999;
27-MAY-1999;
28-MAY-1999;
03-JUN-1999;
                                                                                                                                                                                                                                                                                                            04 - MAX - 1999;
05 - MAX - 1999;
06 - MAX - 1999;
06 - MAX - 1999;
07 - MAX - 1999;
11 - MAX - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                                                                                         25-FEB-2000;
                                                                                                                                                                                                    06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1999;
08-JUN-1999;
10-JUN-1999;
                                                               EP1033405-A2
                                                                                                                                                                                                                                                                               28-APR-1999;
30-APR-1999;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUN-1999;
16-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                            14 -MAY -1999;
18 -MAY -1999;
                                                                                    06-SEP-2000
                                                                                                                                                             23-MAR-1999
25-MAR-1999
                                                                                                                                                                                 29-MAR-1999
01-APR-1999
                                                                                                                                                                                                                                                          23-APR-1999
23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                       14-MAY-1999
14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUN-1999
23-JUN-1999
   The present sequence is the coding sequence of the murine prostate cancer predisposing gene Mm. HPC2, the human homologue of which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs.
                                                                                                                            /*tag= a
/product= "Mm.HPC2"
/partial
/note= "this sequence contains no termination codon"
                                                                                                                                                                                                                                                                                                                                           Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
                               Murine prostate cancer predisposing gene HPC2 coding sequence.
                                                    Mouse; prostate cancer predisposing gene; HPC2; gene therapy; peptide therapy; drug design; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC38171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 AAGGACCCACTGCGACACCTGCGTACGCGGGGGAAGCGCGGGCCG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 LysAspProLeuArgHisLeuArgThrArgGluLysArgGlyPro 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 326 BP; 39 A; 104 C; 127 G; 56 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 20026.
                                                                                                                                                                                                                                                                                          Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AAA60390 from: 1 to: 326
                                                                                                                                                                                                                                                                                        Simard J,
                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 151; 157pp; English
                                                                                                       Location/Qualifiers
51..269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAC38171 standard; DNA; 464 BP.
                                                                                                                                                                                                                                               98US-0107468
                                                                                                                                                                                                                                                                    (MYRI-) MYRIAD GENETICS INC.
                                                                                                                                                                                                                           99WO-US26055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2000 (first entry)
           07-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                        Teng DHF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.00
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US-09-988-687-2 x AAA60390
                                                                                                                                                                                                                                                                                                             WPI; 2000-376481/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
   Quality:
                                                                                                                                                                                                                                                                                                                       P-PSDB; AAB07230
                                                                                                                                                                                WO200027864-A1.
                                                                                                                                                                                                                                                                                        Pavtigian SV,
                                                                                   Mus musculus
                                                                                                                                                                                                                           05-NOV-1999;
                                                                                                                                                                                                                                               06-NOV-1998;
                                                                                                                                                                                                     18-MAY-2000
                                                                                                         Key
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PR 23 - TUN 11999 9905 - 0140955 PR 26 - TUN 11999 1905 - 0140199 PR 26 - TUN 11999 1905 - 014095 PR 26 - TUN 11999 1905 - 0140189 PR 26 - TUN 11999 1905 - 0140189 PR 26 - TUN 11999 1905 - 0140189 PR 26 - TUN 11999 1905 - 0140184 PR 26 - TUN 11999 1905 - 0140186 PR 26 - TUN 11999 1905 - 0140186 PR 26 - TUN 11999 1905 - 0140186 PR 27 - TUN 11999 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1905 - 0140189 1
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Gene signature; messenger RNA; mRNA; relative abundance; frequency;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  511 SerLeuLeuLeuAspCysGlyGluGlyThr 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  200 AGTCTTCTCCTAGATTGTGGTGAAGGAACC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID AAT23314 standard; cDNA to mRNA; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
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                        990S - 0152363
990S - 0153070
990S - 0154018
990S - 0154039
990S - 0154779
990S - 0155486
990S - 0155486
990S - 0155486
990S - 0155486
990S - 0157753
990S - 015929
990S - 015929
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99US-0159331.
99US-0159637.
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990S - 0159584
990S - 0160767
990S - 0160767
990S - 0160814
990S - 0160814
990S - 0160980
990S - 0160980
990S - 0161406
990S - 0161405
990S - 0161359
990S - 0161359
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99US-0161993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0162142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouality: 10.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAC38171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-988-687-2 x AAC38171
01. SEP 11999; 10. SEP 11999; 110. SEP 11999; 116. SEP 11999; 127. SEP 11999; 128. SEP 11999; 128. SEP 11999; 129. SEP 11999; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT23314;
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06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT1901-T25837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Bach library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yeast; germination; proliferation; essential gene; antifungal agent; insecticide; herbicide; anti-proliferation drug; cancer; psoriasis;
                                                                                                                                                                                                                                                            e.g.
non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                        Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAC89621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 161 BP; 30 A; 56 C; 45 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1339-1340; 2245pp; Japanese.
             cell typing; abnormal cell function; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        569 LeuGlyLysProLeuHisProLeuLeu 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AAT23314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 CTGGGCAAACCGCTGCATCCGCTCCTC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recognising different cell types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID AAC89621 standard; DNA; 2517 BP
                                                                                                                94WO-JP01916.
                                                                                                                                         . 93JP-0355504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S. cerevisiae YKR079C gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-988-687-2 x AAT23314/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
human; cloning; mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                                                                                       Okubo K;
                                                                                                                                                                MATSUBARA K.
                                                                                                                                                                                                                             WPI; 1995-206931/27
                                                                                                                                                                (MATS/) MATSUBAR/
(OKUB/) OKUBO K.
                                                                                                                                                                                                       Matsubara K,
                                                                                                                                        12-NOV-1993;
                                                              W09514772-A1
                                                                                                                11-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
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                                                                                      01-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
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                                                                                                                                                                                                                                                                                               tissues
                                       Ношо
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The present invention provides methods of identifying antifungal agents using the coding and protein sequences of several yeast genes. These are essential for the germination and proliferation of Saccharomyces cerevisiae, and include YKR081C, YFR003C, YGR277C, YGR278W, YKR071C, YKR079C and YKR083C. The sequences can also be used to identify compounds for use as herbicides, insecticides and anti-proliferation drugs which can be used in the treatment of cancer, psoriasis and restenosis. This is because they can be used to identify plant, insect and human homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying antifungal compounds which target yeast essential genes comprises use of novel Saccharomyces cerevisiae essential genes YFR003C, YGR277C, YGR278W, YKR0701C, YKR079C or YKR083C or YKR081C
restenosis; YKROB1C; YFROO3C; YGR277C; YGR278W; YKRO71C; YKRO79C;
YKROB3C; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC30375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2517 BP; 881 A; 417 C; 496 G; 723 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             682 LeuLeuIleHisGluAlaThrLeuGlu 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 29; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: AAC89621 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                               (ROSE-) ROSETTA INPHARMATICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
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ID AAC30375 standard; cDNA; 158
                                                                                                                                                                                                                                                                                                                                           99US-0315794.
99US-0389341.
                                                                                                                                                                                                                                                                                  12-MAY-2000; 2000WO-US13017
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                                                                                                              cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 9.00
Ratio: 1.000
Percent Similarity: 100.000
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US-09-988-687-2 x AAC89621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-025092/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the yeast genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB49964
                                                                                                                                                                    WO200071161-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; 5' EST;
                                                                                                              Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                           21-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                         02-SEP-1999;
                                                                                                                                                                                                                             30-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roberts CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
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Human; secreted protein, EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; antiinflammatory; tumour inhibition; antitumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 Fragments (AAT18674-76) of a human trophinin cDNA clone (AAT1867 code for active, exposed cell surface domains (AAR94897-99, respectively), of trophinin. These domains contain regions of hydrophilic decapeptide repeats. Protein secondary structure algorithms predict that the decapeptide repeats conform to a repeated beta-turn structure, which may be involved in homophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein 5' EST SEQ ID NO: 154 from WO 9906553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalian trophinin and trophinin-assisting protein - used inhibiting or enhancing embryo implantation, diagnosis of infertility and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX41495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 8
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 216 BP; 36 A; 66 C; 54 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                            (LJOL-) LA JOLLA CANCER RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 MetAlaProAlaSerValLeuVal 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 21; Fig 3; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 ATGGCACCAGCCTCTGTTTGGTG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX41495 standard; cDNA; 384
                                                                                                                                                                                                                                                                                                            95US-0439818.
                                                                                                                                                                                                                                                                     95WO-US13259
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                 g
                                                               o
                                                        /*tag= e
151..180
                                                                                               /*tag= f
181..210
                                  121.150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AAT18675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 1.000
Percent Similarity: 100.000
                                                                                                                                           /*tag=
                 /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-209192/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR94898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                    W09610414-A1
                                                                                                                                                                                                                                                                   04-OCT-1995;
                                                                                                                                                                                                                                                                                                                                  04-OCT-1994;
                                                                                                                                                                                                                                                                                                            .2-MAY-1995;
                                       repeat_unit
                                                                                repeat_unit
repeat_unit
                                                                                                                       repeat_unit
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                                                                                                                                                                                                                                                                                                                                                                                                                   Pukuda MN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX41495;
The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length CDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trophinin; trophinin-assisting protein; tastin; bystin; lastin; embryo implantation; infertility; cell adhesion; therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1996.DAT:AAT18675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 158 BP; 20 A; 54 C; 47 G; 37 T; 0 other;
                                                                                                                                           Giordano J;
                                                                                                                                                                                                                                                                                                            claim 1; SEQ ID 34450; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human trophinin external domain 2 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AAC30375
                                                                                                                                           Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470 GlyProAlaProAlaGluLysArg 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 GGTCCAGCTCCTGCTGAGAAGCGC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT18675 standard; cDNA; 216
             21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-988-687-2 x AAC30375/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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Ratio: 1.000
Percent Similarity: 100.000
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31..60
/*tag=
61..90
/*tag=
                                                                                                                                           Dumas Milne Edwards J,
                                                                                                                                                                                WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                  (GEST ) GENSET
                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-JUL-1996
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to: 216

Key

(AAT18673)

in

Giordano J;

Duclert A,

99US-0122487

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21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                       Dumas Milne Edwards J,
                                                                                                                                                                                                             (GEST ) GENSET
                                                                                                                                                                   26-FEB-1999;
                                       EP1033401-A2
  Homo sapiens
                                                                                 06-SEP-2000.
human secreted proteins, and encode the proteins given in AAX12521 to human secreted proteins, and encode the proteins given in AAX12521 to AAX12568, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for products for diagnosis and therapy. The proteins obtained may have crytokine activity, cell proliferation/differentiation activity, vell proliferation/differentiation activity, reproductive hormone activity, tissue growth regulating activity, reproductive hormone regulating activity, receptor/ ligand activity, antiinflammatory activity, tumour inhibition activity or other activity, antiinflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping promoter sequences. The nucleic acids encoding the signal peptide can be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for obtaining extracellular secretion of a polypeptide into a membrane, or importing a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding human secreted proteins - obtained from cDNA libraries derived from umbilical cord, lymph ganglia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC27730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 384
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                             Lacroix
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                                                                                                                                                                                                                                                                           Duclert A, Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to reverse of: AAX41495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 271; 411pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocytes and placental tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358 TTGAGGTCAGCCGCAGGAAGAACT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAC27730 standard; cDNA; 425 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LeuArgSerAlaAlaGlyArgThr 15
                                                                                                                                             98WO-IB01237
                                                                                                                                                                                       97US-0905051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-988-687-2 x AAX41495/rev
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Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                WPI; 1999-153783/13.
P-PSDB; AAY12637.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                               (GEST ) GENSET
                                                           WO9906553-A2.
                   Homo sapiens
                                                                                                                                             31-JUL-1998;
                                                                                                                                                                                       01-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000
                                                                                                     11-FEB-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                            New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used to obtain full length cDNAs and genomic DNAs. 5' ESTs ar
in diagnostic, forensic, gene therapy and chromosome mapping
They are used to obtain upstream regulatory sequences and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 425 BP; 127 A; 66 C; 115 G; 108 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 8
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                     Claim 1; SEQ ID 31805; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: AAC27730 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    733 ProLeuPheSerProAsnPheSer 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 CCGCTTTTCTCGCCAAACTTCAGT 346
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Percent Similarity: 100.000
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US-09-988-687-2 x AAC27730
WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
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BC007619 Homo sapiens, clon
1 AC049359 Glardia intestinal
AF038408 Streptcalloteichus
BC008146 Homo sapiens, clon
AF053070 Homo sapiens NADH:
1 Y17383 Homo sapiens NADH:
1 AR137565 Sequence 51 from p
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Eutheria; Primates; Catarrhin; Hominidae; Homo.

Anamalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

E 1 (bases 1 to 2908)

Tavtigian, S.V., Simard, J., Teng, D.H.E., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Latty, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Santh, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A. Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p 1175785

E 2 (bases 1 to 2908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="Aag24441.1"
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ENEPHLPHGVSQRRGVRDSSLVVAFICKLHLKRGNFLVLKAKEMGLPVGTAAIAPIIA
AVKDGKSITHEGREILAEELCTPPDPGAAFVVVECPDESFIQPICENATFQRYQGKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPDIFPLLTSFRCKKEGPTLSVPMVQGECLLKYQLRPRREWQRDAITTCNPEEFIVEA
LQLPNFQQSVQEYRRSAQDGPAPAEKRSQYPELIFLGTGSAIPWKIRNVSATLVNISP
DTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERAL
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ISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATL
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EKVGVAFDHMKVCFGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSRE
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HPC2/ELAC2"
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/db_xref="taxon:9606"
/chromosome="17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 1 AC003694 Mus musculus chrome

15 AE003694 Rhizobium meliloti

16 G26261 human STS TGR-A002317,

17 AC029747 Giardia intestinalis of

18 AC032553 Giardia intestinalis of

18 AC08618 Giardia intestinalis of

18 AC06132 Giardia intestinalis of

18 AC06132 Giardia intestinalis of

18 AC030275 Giardia intestinalis of

18 AC040707 Giardia intestinalis of

18 AC070405 Giardia intestinalis of

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1 ALIS8046 Human DNA sequence
1 AP001550 Oryza sativa genomi
1 AC055736 Homo sapiens 12 BAG
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AF304370 Homo sapiens putativi BC001939 Homo sapiens, putati BC004158 Homo sapiens, putati
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AL39555 T3 end of clone ASOAA(
ACO84975 Giardia intestinalis c
ACO64766 Giardia intestinalis c
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                                                                                                                                                                                    -WODEL-frame+p2m.model -DEV=x1h
-Q-Cgn2_1/USPTO_spool/VS0988687/runat_29032002_092149_570/app_query.fasta_1.895
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-USER-USG9988687_CGGN1_17060 -NCPU=6 -LICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000 WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT-XGAPEXT=60.000
                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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    out_format : pfs
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89
  OM of: US-09-988-687-2 to: GenEmbl:*
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Database sequences: 1472140
Database length: -341344837
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                                                 6:33
                                                                                                                                                                Command line parameters:
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Query length: 826
                                                 Date: Mar 29, 2002
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gb_htg:AC070405
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gb_htg:AC064766
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Jb_pr:AF304370
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gb_pr:BC004158
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euPheAsnCysGlyGluGlyValGlnArgLeuMetGlnGluHisLysLeu 100 roLysCysValLeuSerGlyProProGlnLeuGluLysTyrLeuGluAla 150 rGlnGlyArgThrIleSerGlnAlaProAlaArgArgGluArgProArgL ysaspProLeuargHisLeuargThrargGluLysargGlyproSerGly CAAAGTGTGTTTTCTGGACCTCCACAACTGGAAAATACCTCGAAGCA alArgAspSerSerLeuValValAlaPheIleCysLysLeuHisLeuLys MetTrpAlaLeuCysSerLeuLeuArgSerAlaAlaGlyArgThrMetSe AGGACCCGCTGCGCACCTGCGCACGCGAGAGCGCGGGACCGTCGGGG CysSerGlyGlyProAsnThrValTyrLeuGlnValValAlaAlaGlySe rArgAspSerGlyAlaAlaLeuTyrValPheSerGluPheAsnArgTyrL TCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA IleLysIlePheSerGlyProLeuLysGlyIleGluLeuAlaValArgPr OHisSerAlaProGluTyrGluAspGluThrMetThrValTyrGlnIleP rolleHisSerGluGlnArgArgGlyLysHisGlnProTrpGlnSerPro GluArgProLeuSerArgLeuSerProGluArgSerSerAspSerGluSe rAsnGluAsnGluProHisLeuProHisGlyValSerGlnArgArgGlyV Identity: 100.000 LAGGLEDGEPQQKRAHTEEPQAKKVRAQ" Gaps: to: б Percent from: 1 O Ratio: 1.000 Percent Similarity: 100.000 to: AF304370 826.00 US-09-988-687-2 x AF304370 ø Quality: Ratio: alignment_scores alignment_block Align seg 1/1 BASE COUNT -0.1 ORIGIN

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                     ArgGlyAsnPheLeuValLeuLysAlaLysGluMetGlyLeuProValGl
                                  yThrAlaAlaIleAlaProIleIleAlaAlaValLySASpGlyLySSerI
                                                                             leThrHisGluGlyArgGluIleLeuAlaGluGluLeuCysThrProPro
                                                                                                                          AspProGlyAlaAlaPheValValValGluCysProAspGluSerPheIl
                                                                                                                                                                                   GATCCTGGTGCTGCTTTTGTGGTGGTGGAATGTCCCAGATGAAAGCTTCAT
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1601 GGGTCCTGGCACCCTGGCTGTGTTTGTGTCCCACCTGCACGAGAT 1650

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ACCESSION
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                                        651 CysalaLeuValHisThrSerGlyTrpLysValValTyrSerGlyAspTh
                    HisHisThrGlyLeuProSerIleLeuLeuGlnArgGluArgAlaLeuAl
                                                                                                    567 aSerLeuGlyLysProLeuHisProLeuLeuValValAlaProAsnGlnL
                                                                                                                                                                                        584 euLysAlaTrpLeuGlnGlnTyrHisAsnGlnCysGlnGluValLeuHis
                                                                                                                                                                                                                                                                            HislleSerMetileProAlaLysCysLeuGlnGluGlyAlaGluIleSe
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2997 bp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov series: TRAL Plate: 9 Row: i Column: 17 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-JAN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Homo sapiens, putative prostate cancer susceptibility protein, clone MGC:4102 IMAGE:2820640, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2997)
Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                            BC001939.1 GI:12804972
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S

us-09-988-687-2.olip2n.rge

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 2 Row: c Column: 13 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3006)
Strausberg, R.
                                                                                                                                            Submitted (01-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .3006
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/lab_host="NHING-7"
                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: porB7" 70. .2550
                                                                                                                                                                                                                                                                                                     Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                808 c
                                                                                                                            Direct Submission
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0.879
99.879
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Ratio:
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TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2361 GAAAGCCCTGTTTGCTGGCGACATCGAGGAGGAGGAGGAGGAGGAGA 2410
                                                                                                    2161 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGC 2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2411 AGCGGGAGCTGCGGCAGGTGCGGGCGGCCCTCTGTCCAGGGAGCTGGCA 2460
                                     1761 ATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCCCCCAACCAGC 1810
                                                                                                                                                                                                                                                                                                                                                                                                                             667
                                                                                                                                                                                                                                                      634
                                                                                                                                                                                                                                                                                                                                         euGluGluPheGlnThrCysLeuValArgHisCysLysHisAlaPheGly 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      734 euPheSerProAsnPheSerGluLysValGlyValAlaPheAspHisMet 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysValCysPheGlyAspPheProThrMetProLysLeuIleProProLe 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uLysAlaLeuPheAlaGlyAspIleGluGluMetGluGluArgArgGluL 784
                                                                                                                                                                                                                                                                                                                                                               701 ThrHisSerThrThrSerGlnAlalleSerValGlyMetArgMetAsnAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ysArgGluLeuArgGlnValArgAlaAlaLeuLeuSerArgGluLeuAla
                                                                             584 euLysAlaTrpLeuGlnGlnTyrHisAsnGlnCysGlnGluValLeuHis
                                                                                                                                                                                                                                                    617 rSerProAlaValGluArgLeuIleSerSerLeuLeuArgThrCysAspL
                                                                                                                                                                                                                                                                                                                                                                                                                           CysAlaLeuValHisThrSerGlyTrpLysValValTyrSerGlyAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    717 aGluPhelleMetLeuAsnHisPheSerGlnArgTyrAlaLysValProL
                                                                                                                                                                  HislleSerMetIleProAlaLysCysLeuGlnGluGlyAlaGluIleSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2511 GCCACAGGCCAAGAAGGTCAGAGCCCAG 2538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    817 uProGlnAlaLysLysValArgAlaGln 826
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LOCUS
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be found

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1 MetTrpAlaLeuCysSerLeuLeuArgSerAlaAlaGlyArgThrMetSe 17
                                                                                                        Length: 826
Gaps: 0
Percent Identity: 99.879
                                                                                                                                            to: 3006
                                                                                б
                                                                                                                                            from: 1
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119	34 169	50 219	67 269	84 319	100 369	117	134 469	150	167	184 619	200	217	234	250 819	267 869	284	300	317
	rGlnGlyArgThrileSerGlnAlaProAlaArgArgGluArgProArgL 	ysaspproleuarghisteuargthrarglulysargglyprosergly	1 CysSerGlyGlyProAsnThrValTyrLeuGlnValValAlaalaGlySe (7 rArgAspSerGlyAlaAlaLeuTyrValbheSerGluPheAsnArgTyrL	4 euPheasnCysGlyGluGlyValGlnArgLeuMetGlnGluHisLysLeu :	1 LysvalalaargLeuaspasnIlePheLeuThrargMetHisTrpSeras	7 nValGlyGlyLeuSerGlyMetlleLeuThrLeuLysGluThrGlyLeuP :	4 roLysCysvalLeuSerGlyProProGlnLeuGluLysTyrLeuGluala 	1 IleLysIlePheSerGlyProLeuLysGlyIleGluLeuAlaValArgPr	7 OHISSERAlaProGluTyrGluAspGluThrMetThrValTyrGln1leP	4 rolleHisSerGluGlnArgArgGlyLysHisGlnProTrpGlnSerPro :	1 GluargProLeuSerargLeuSerProGluargSerSerAspSerGluSe :	7 rasnGluasnGluProHisLeuProHisGlyValSerGlnArgArgGlyV :	4 alargaspserSerLeuValValalaPheIleCysLysLeuHisLeuLys 	1 ArgGlyAsnPheLeuValLeuLySAlaLysGluMetGlyLeuProValGl :	7 yThrAlaAlaIleAlaProIleIleAlaAlaValLysAspGlyLysSerI	leThrHisGluGlyArgGluIleLeuAlaGluGluLeuCysThrProPro	01 AspProGlyAlaAlaPheValValGluCysProAspGluSerPheIl :
7.0	17	34	22	27	32	10 37	111	13,47,	15	16 57	18	20	21	23,	25	26.	284	30

970	GATCCTGGTGCTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCAT]	1019
317	3lnProlleCysGluAsnAlaThrPheGlnArgTyrGlnGlyLysAlaA	334
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351	ASPSerargTyrGlnGlnTrpMetGluargPheGlyProaspThrGlnHi	367 1169
367	SLeuValLeuAsnGluAsnCysAlaSerValHisAsnLeuArgSerHisL	384
384	ysileGlnThrGlnLeuAsnLeuIleHisProAspIlePheProLeuLeu (400
401	ThrSerPheArgCysLysLysGluGlyProThrLeuSerValProMetVa 4	417
417	GlnGlyGluCysLeuLeuLysTyrGlnLeuArgFroArgArgGluTrpG	434
434	InargaspalaileIleThrCysasnProGluGluPheIleValGluala 4 	450
451	LeuGhnLeuProAsnPheGhnGhnSerValGhnGhuTyrargArgSerAl 4	467
467	aGInAspGlyProAlaProAlaGluLysArgSerGlnTyrProGluIleI 4 	484
484	lePheLeuGlyThrGlySerAlaIleProMetLysIleArgAsnValSer	500 1569
501 1570	AlaThrLeuValAsnIleSerProAspThrSerLeuLeuLeuAspCysGl 5 	517
517	yGluGlyThrPheGlyGlnLeuCysArgHisTyrGlyAspGlnValAspA 5 	534
534	rgValLeuGlyThrLeualaalaValPheValSerHisLeuHisAlaAsp 5 	550
551 1720	HisHisThrGlyLeuProSerIleLeuLeuGlnArgGluArgAlaLeuAl 5 	567 1769
567 1770	aSerLeuGlyLysProLeuHisProLeuLeuValValAlaProAsnGlnL 5 	584 1819
584	euLysalaTrpLeuGlnGlnTyrHisasnGlnCysGlnGluValLeuHis (600
601 1870	HislleSerMetlleProAlaLySCysLeuGlnGluGlyAlaGlulleSe (617 1919

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Percent Identity: 99.602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product"
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1. .2976
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                                                                                                                                                                                                                                                                                                                  University of Tokyo
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US-09-988-687-2 x AK001392
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REFERENCE
AUTHORS
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TITLE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H., Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligo capping; fis [full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
clone_lib:NT2RP2 clone:NT2RP2000985.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2470 GGGGGCTGGAGGATGGGGAGCCTCACCAGAAGCGGGCCCACACAGAGGA 2519
                         1920 CAGTCCTGCAGTGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATT 1969
                                                                                                                           2019
                                                                                                                                                                                                                                               2170 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGC 2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2370 GAAAGCCCTGTTTGCTGGCGACATCGAGGAGATGGAGGAGCGCAGGGAGA 2419
                                                                                                                                                                                                                                                                                                                                                                           2120 TACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAAG 2169
                                                                                                                                                                    667
                                                                                                                                                                                                                                                                                                                                      700
                                                                                    650
                                                                                                                                                                                                                                                                                                                                                                                                                    701 ThrHisSerThrThrSerGlnAlaIleSerValGlyMetArgMetAsnAl 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    717 aGluPheIleMetLeuAsnHisPheSerGlnArgTyrAlaLysValProL 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   734 euPheSerProAsnPheSerGluLysValGlyValAlaPheAspHisMet 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   751 LysValCysPheGlyAspPheProThrMetProLysLeuIleProProLe 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   767 uLysalaLeuPhealaGlyaspileGluGluMetGluGluArgargGluL 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK001392 2976 bp mRNA PRI 2
Omno sapiens cDNA FLJ10530 fis, clone NT2RP2000985,
AK001392.1 GI:7022621
                                                                                                         2020 TGTGCGCTGGTGCACACCTCTGGCTGGAAAGTGGTCTATTCCGGGGACAC
                                                                                                                                                                                                                                                                                                                                 684 1eHisGluAlaThrLeuGluAspGlyLeuGluGluGluAlaValGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2270 TCTTCAGCCCCAACTTCAGCGAGAAAGTGGGGAGTTGCCTTTGACCACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2420 AGCGGGAGCTGCGGCAGGTGCGGCGCCCTCCTGTCCAGGGAGCTGGCA
  617 rSerProAlaValGluArgLeuIleSerSerLeuLeuArgThrCysAspL
                                                                                    euGluGluPheGlnThrCysLeuValArgHisCysLysHisAlaPheGly
                                                                                                                                                                  651 CysAlaLeuValHisThrSerGlyTrpLysValValTyrSerGlyAspTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   784 ysArgGluLeuArgGlnValArgAlaAlaLeuLeuSerArgGluLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 GlyGlyLeuGluAspGlyGluProGlnGlnLysArgAlaHisThrGluGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             817 uProGlnAlaLysLysValArgAlaGln 826
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LOCUS          AK001392
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VERSION
KEYWORDS
SOURCE
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Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T. NEDO human cDNA sequencing project

NEDO human cDNA sequencing project

2 (bases 1 to 2076)

E 2 (bases 1 to 2076)

E 1 (bases 1 to 2076)

E 2 (bases 1 to 2076)

E 2 (bases 2 to 2076)

E 3 (bases 2 to 2076)

E 3 (bases 2 to 2076)

E 4 (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao 1 sogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3952)

E 5 (bases 2014, Fax:81-48-52-3952)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Blotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / VOD_XERE=""" VOLZO 12.2."
/ TEARS 1 at 1.0 n = "WWALCELLRSAAGRTMSOGRTISOAPARRERPRKDPLRHLRTRE
/ KRGPSGCSGGPNTVYLQVVAAGSRDSGAALYVFSEFNRYLFNCGEGVORLMOEHKLKV
ARLDNIFTERMWRWSNGGLSGNILTLKERGTERKYLEPROFPGGERYLEAKIFSOELKG
IELAMRPHGAPEY EDDETWYVO 1PTHSEGRRGKHOPWOSPERPLSE AKTSFOELKG
IELAMRPHGAPEY EDDETWYVO 1PTHSEGRRGKHOPWOSPERPLSE AKSPERSESDSESN
ENEPHLPHGVSORRGVRDSSLVVAFICKLHLKRGNFLVLKAKEMGLPVGTAAIAPIIA
AVKDGKSTITHGREELLAFEELCTPPPDFGAARVVVEDDESSIQPFCENATFORYOGKAD
APVALVVHAAPASVLUNDSRYQOWMERGEPDTOHLVLNANCASITHGRYGORAD
APVALVVHAAPASVLUNDSRYQOWMERGEPDTOHLVLNANCASITHGRYGGASD
APVALVVHAAPASVLUNDSRYQOWNEGTLAKVQLRPREWORDAITCNPEFILVAISPD
TSLLLDCGEGTFGOLCRHYGDOVDRVLGTLAAVFVSHLHADHHTGLPSILLQRERALA
SLGKREHPLLVVAPNOLLKAMLOQYYNGCQEVLHHISMIPAKCLOGGAEISSPAVERLI
SSLLRTCDLEEFGYCLVRHKGHAFGCALVHTSGWKVYSGOTMPCEALVRAGKDATLL
IHBATLEDGLEEEBAVEKTHSTTSQAISVGRWARAETIMLNHFSGRYAKVPLFSPNFSE
KVGYAFDHWKVCLGOPPTHRKLIPPLKALFAGDIEEBERRERERRORTLL
AGGLEDGSLSRSGFTORSHRPRERSESEDLGDPELRRLCVFCPTHAPVSALLSREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="cloning vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 rGlnGlyArgThrIleSerGlnAlaProAlaArgArgGluArgProArgL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetTrpAlaLeuCysSerLeuLeuArgSerAlaAlaGlyArgThrMetSe 17
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TyrLeuGlnValValAlaAlaGlySe 67	rValPheSerGlubheAsnArgTyrt 84	lnArgLeuWetGlnGluHisLysLeu 100	PheLeuThrargMetHisTrpSerAs 117	eLeuThrLeuLysGluThrGlyLeuP 134	roGlnLeuGluLysTyrLeuGluAla 150 .	GlylleGluLeuAlaValArgPr 16	pGluThrMetThrValTyrGlnIleP 184	lyLysHisGlnProTrpGlnSerPro 200	ProGluArgSerSerAspSerGluSe 217	OHISGIYVAlSerGlnArgArgGlyV 234	laPhelleCysLysLeuHisLeuLys 250	AlaLysGluMetGlyLeuProValGl 267	ealaalavallysaspGlyLysseri 284	eualagludluLeuCysThrProPro 300	ValGluCysProAspGluSerPhell 317	rPheGlaargTyrGlaGlyLysalaa 334	isMetalaBroalaGerValLeuVal 350
51 CysSerGlyGlyProAsnThrVal'	67 rArgAspSerGlyAlaAlaLeuTy:	84 euPheAsnCysGlyGluGlyValG:	101 LysvalalaargLeuAspasnileE	117 nValGlyGlyLeuSerGlyMetIle	134 roLyscysValleuSerGlyProPi	151 IleLysIlePheSerGlyProLeulys	167 OHISSERALAPROGLUTYRGLUAS	184 rolleHisSerGluGlnArgArgG	201 GluargProLeuSerargLeuSeri	217 rAsnGluAsnGluProHisLeuPro	234 alArgAspSerSerLeuValValA	251 ArgGlyAsnPheLeuValLeuLysAla	267 yThralaalailealaproileile	284 leThrHisGluGlyArgGluIleLv	301 AspProGlyAlaAlaPheValValV	317 eGlnProlleCysGluAsnAlaThri	334 spAlaProvalAlaLeuValValHi

351	ASPSerArgTyrGlnGlnTrpMetGluArgPheGlyProAspThrGlnHi 367 	67 174
367	sLeuValLeuAsnGluAsnCysAlaSerValHisAsnLeuArgSerHisL 384	84
384	ysileGinThrGinLeuasnLeuileHisProaspilePheProLeuLeu 400	27.4
401	ThrSerPheArgCysLysGluGlyProThrLeuSerValProMetVa 417	7 2
417	GlnGlyGluCysLeuLeuLysTyrGlnLeuArgProArgArgGluTrpG 434 	34
434	InargaspalarlerlerhrcysasnProGluGluPherleValGluala 450 	50
451	LeuGhnLeuProAsnPheGinGinSerValGinGluTyrargargseral 467 	67 471
467	aGlnAspGlyProAlaProAlaGluLysArgSerGlnTyrProGlulle1 484	34 521
1522	lePheLeuGlyThrGlySerAlaIleProMetLySIleArgAsnValSer 500	571
501 1572	AlaThrLeuValAsnIleSerProAspThrSerLeuLeuLeuAspCysGl 517 	17
517	yGluGlyThrPheGlyGlnLeuCySArgHisTyrGlyAspGlnValAspA 534	34
534	rgValLeuGlyThrLeualaAlaValPheValSerHisLeuHisAlaAsp 550 	50
551	HisHisThrGlyLeubroSerIleLeuLeuGlnargGluargAlaLeuAl 567	57 171
567	aSerLeuGlyLysProLeuHisProLeuLeuValValAlaProAsnGlnL 584	34 321
584	eulysalaTrpLeuGlnGlnTyrHisasnGlnCysGlnGluValLeuHis 600 	30 371
601 1872	HislleSerMetlleProAlaLysCysLeuGlnGluGlyAlaGluIleSe 617 	17 921
617	rSerProAlaValGluArgLeulleSerSerLeuLeuArgThrCysAspL 634	34 971
634	euGluGluPheGlnThrCysLeuValArgHisCysLysHisAlaPheGly 650 	50
651	CysAlaLeuValHisThrSerGlyTrpLysValValTyrSerGlyAspTh 667	57

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225 roHisGlyValSerGlnArgArgGlyValArgAspSerSerLeuValVal 241
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Percent Similarity: 100.000
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US-09-988-687-2 x AF308698
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                                                                                                                                                                                  CDS
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S Tavtigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Ilev, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A., A candidate prostate cancer susceptibility gene at chromosome 17p 11175785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Laity, K., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schoeder, M., Snith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Wodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
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2022 TGTGCGCTGGTGCACACCTCTGGCTGGAAGTGGTCTATTCCGGGGACAC 2071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2222 GGAGTTCATTATGCTGAACCACTTCAGCCAGCGCTATGCCAAGGTCCCCC 2271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2122 TACATGAAGCCACCCTGGAAGATGGTTTGGAAGAGGAAGCAGTGGAAAG 2171
                                                                                                                                                                                                                                                                                                                                                               2172 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGC 2221
                                                                                                                                                                                                                                                                                                                                717
                                                                                                                                                                                                           684 leHisGluAlaThrLeuGluAspGlyLeuGluGluGluAlaValGluLys 700
                                                                                                                                                                                                                                                                                                                                                                                                                                               717 aGluPhelleMetLeuAsnHisPheSerGlnArgTyrAlaLysValProL 734
                                                                                                                                                                                                                                                                                                                             701 ThrHisSerThrThrSerGlnAlaIleSerValGlyMetArgMetAsnAl
                                                                                         rMetProCysGluAlaLeuValArgMetGlyLysAspAlaThrLeuLeuI
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AF308698
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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AUTHORS
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/UL-ALL STANDAY STANDA
Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt Lake City, UT 84103, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 spGluThrMetThrValTyrGlnIleProIleHisSerGluGlnArgArg 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 GlnArgLeuMetGlnGluHisLysLeuLysValAlaArgLeuAspAsnIl
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788 c 819 g 589 t
                                                                                                                                                                                                              /organism="Pan troglodytes"
/db_xref="taxon:9598"
1. .2481
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                                                                                                                                                                                                                                                                                                                                                                                                       /product="ELAC2"
/protein_id="AAG24920.1"
/db_xref="G1:10946497"
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PHIGHER TO THE STANDARD THE STA
                                                                                                                                                              Direct Submission
Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, 07 84103, USA
Location/Qualifiers
Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
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Gaps: 1
Percent Identity: 99.422
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                                                                                                                                                                                                                                                                                                 1. .2893
/organism="Gorilla gorilla"
/db_xref="taxon:9593"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="ELAC2"
                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ELAC2"
1. .2481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="ELAC2"
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99.422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Cartilo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Camilo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., M., Cupte, J.S., Hu, K., Illev, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Woodland, A.M., Labrie, E., Skolinck, M.H., Neuhausen, S., Rommens, J., and Cannon Albright, L.A.
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                                                                                                        sAlaLysGluMetGlyLeuProValGlyThrAlaAlaIleAlaProIleI 275
                                                                                                                                                                                                                                                                      lValGluCysProAspGluSerPheIleGlnProIleCysGluAsnAlaT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuAlaGluGluLeuCysThrProProAspProGlyAlaAlaPheValVa 308
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Gorilla gorilla ELAC2 (ELAC2) mRNA, complete cds.
AF308694
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Tavtigian, S.V., Siman
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LOCUS AF308694
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SOURCE
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2 (bases 1 to 118788)

Birren, B., Feaman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Bottwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E., Dewon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., Deyon, K., Geradgery, K., Gilmartin, T., Gradyna, S., Gersheimer, S., Geradgery, K., Gilmartin, T., Gradth, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Machan, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nachman, A., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Stone, C., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission

Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 118788)

Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Badnin, J., Boatin, C., Boutwell, C., Brown, A., Carle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, L., Etemadi, S., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gensheimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kann, L., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Machman, A., Nahf, R., Nayler, J., Morris, W., Morrow, J., Mythaleck, T., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Strickland, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Only the first 118.8 kilobases of this clone are being submitted The remainder overlaps accession number AC005274 (WICGR project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Ge Research, 320 Charles Street, Cambridge, MA 02141, USA on Jul 23, 1998 this sequence version replaced gi:3335015. All repeats were identified using RepeatMasker: Smit, A.F.A. Green, P. (1996-1997)
                      Birren, B., Fasman, K., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone hRPK.597_M_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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/clone_lib="RPCI-11 human BAC library"
/map="17"
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1. .118788
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/rpt_family="AT_rich"
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/rpt_family="MER34"
2718. .3477
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/rpt_family="MIR"
complement(932. .1
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/rpt_family="L2"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LysValAlaArgLeuAspAsnIlePheLeuThrArgMetHisTrpSerAs 117
                                                 OHisSerAlaProGluTyrGluAspGluThrMetThrValTyrGlnIleP 184
                                                                                                                                                                                                                                                                                                                                                                                                                                  234 ValArgAspSerSerLeuValValAlaPheIleCysLysLeuHisLeuLy 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sArgGlyAsnPheLeuValLeuLysAlaLysGluMetGlyLeuProValG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 lyThrAlaAlaIleAlaProIleIleAlaAlaValLysAspGlyLysSer 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oAspProGlyAlaAlaPheValValValGluCysProAspGluSerPheI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            900 AGATCCTGGTGCTTTTTGTGGTGGTAGAATGTCCAGATGAAAGCTTCA 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 leGlnProIleCysGluAsnAlaThrPheGlnArgTyrGlnGlyLysAla 333
                                                                                                                     nValGlyGlyLeuSerGlyMetIleLeuThrLeuLysGluThrGlyLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rolleHisSerGluGlnArgArgGlyLys.HisGlnProTrpGlnSerPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AspAlaProValAlaLeuValValHisMetAlaPro 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC005277.1 GI:3337311
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complement (5963: .6275)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20816. .25895
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/note="Single-stranded coverage."
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26312. .26337
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/rpt_family "L2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="MER218"
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complement(20821, .21069)
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Ratio: 1.000
Percent Similarity: 100.000
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67 rArgAspSerGlyAlaAlaLeuTyrValPheSerGluPheAsnArg 82

ORGANISM

REFERENCE AUTHORS

ACCESSION

VERSION KEYWORDS SOURCE

sed_name:

JOURNAL PUBMED REFERENCE

TITLE

AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

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LÜVHIAPESULIDSRYOOWMERFGPDTOHLILNENCPSUHNLRSHKIOTÖLSLIHPDI
FPOLTSEYSKEGSTLLSYPTYRGECLLKYOLRSPKREWGNDTPPDCNTDEFLARALELP
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ATLEDGLEERAVERTHSTRSQA INVGARMANGGFIALHE
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IAFDHMKVCFGDFPTVPKLIPPLKALFAGGIEEMVERREKRELRLVRAALLTQQADSP
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1 (bases I to 740)

Tavtigian, S. V., Simard, J., Teng, D. H. F., Baumgard, M., Beck, A., Camp, N. J., Carillo, A. R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J. M., Frank, D., Frye, C., Ghaffari, S., Gupte, J. S., Hu, R., Illev, D., Janecki, T., Kort, E. N., Laity, K. E., Leavitt, A., Leblanc, G., McArthur-Worrison, J., Pederson, A., Penn, B., Peterson, K. T., Reid, J. E., Richards, S., Schroeder, M., Smith, R., Snyder, S. C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 GlyMetIleLeuThrLeuLysGluThrGlyLeuProLysCysValLeuSe 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        357 GGAATGATTTTAACTTTAAAGGAAACCGGGCTTCCCAAATGTGTTCTGTC 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 rGlyProProGlnLeuGluLysTyrLeuGluAlaIleLysIlePheSerG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 lyProLeuLysGlyIleGluLeuAlaValArgProHisSerAlaProGlu 172
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/note="similar to Homo sapiens HPC2/ELAC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 51
Gaps: 0
Percent Identity: 100.000
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741 c 748 g 564 t
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                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   507 TAC 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SEGMENT
             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Lo 2712)

1 (bases 1 to 2712)

2 Tavtigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Lalty, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p in the state of the sta
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Submitted (27-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt-Lake City, UT 84103, USA
4 (bases 1 to 2712)
Tavtigian,S.V., Simard,J., Teng,D.H.F., Baumgard,M., Beck,A., Camilo,A.R., Chen,Y., Dayanath,P., Desrochers,M., Dumont,M., Farnham,J.M., Frank,D., Trye,C., Ghaffari,S., Gupte,J.S., Hu,R., Iliev,D., Janecki,T., Kort,E.N., Latty,K.E., Leavitt,A., Leblanc,G., McArthur-Morrison,J., Pederson,A., Penn,B., Peterson,K.T., Raid,J.E., Richards,S., Schroeder,M., Smith,R., Sonyder,S.C., Swedlund,B., Swensen,J., Thomas,A., Tranchant,M., and Cannon,Albright,L.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. (bases) to 2712)
Tavtidian, S. V., Simard, J., Teng, D. H.F., Baumgard, M., Beck, A.,
Tavtidian, S. V., Simard, J., Teng, D. H.F., Baumgard, M., Berchers, M.,
Dumont, M., Farnham, J. M., Frank, D., Frye, C., Ghaffari, S.,
Gupte, J. S., Hu, R., Iliev, D., Janecki, T., Kort, E. N., Laity, K.E.,
Leavitt, A., Leblanc, G., McArthur-Worrison, J., Pederson, A., Penn, B.,
Breterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R.,
Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M.,
and Cannon-Albright, L.A., Skolnick, M.H., Neuhausen, S., Rommens, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 2712)
2 (bases 1 to 2712)
2 (bases 1, Sumard, J., Teng, D.H.F., Baumgard, M., Beck, A., Cartiglo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Cupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, En., Lieavitt, A., Leblanc, G., MoArthur-Morrison, J., Pederson, A., Penn, B., Sander, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
                                                                                                                                                                                                                                                                      27-FEB-2001
ROD
                                                                                                                                                                                                                                  AF308696 2712 bp mRNA
Mus musculus ELAC2 mRNA, complete cds.
AF308696
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/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                            AF308696.2 GI:11992378
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                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AF308696
DEFINITION Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                   gb_ro:AF308696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
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source

FEATURES REMARK

COMMENT

TITLE JOURNAL

TITLE JOURNAL

REFERENCE AUTHORS

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Ratio: 1.000
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                           Unpublished
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Ratio:
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 human
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                                                                    REFERENCE
                                                                                    AUTHORS
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                                                                                                                                                                                                                                          TITLE
SOURCE
                                                                              Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Canillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Luk, T., Hu, R., Ilaev, D., Janecki, T., Kort, E.N., Latty, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Raid, J.E., Richards, S., Schroeder, M., Smith, R., Woodland, A.M., Labrie, F., Swensen, J., Thomas, A., Tranchant, M., and Cannon, Albright, L.A.
                                                                                                                                                                                                                                                     Direct Submission
Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 84108, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="PDTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLAAVFVSHLHADH
                                                                                                                                                                                                                                                                                                                                                                                                                                                     <301. .>439
/product="putative prostate cancer susceptibility protein
HPC2/ELAC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
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                                strong candidate prostate cancer susceptibility gene at
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="17"
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/db_xref="G1:10880931"
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US-09-988-687-2 x AF304371S2
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                                                  chromosome 17p
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LOCUS AF304371S1
                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       exon
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                                                                    JOURNAL
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KEYWORDS
SEGMENT
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                                                                                                                                                                                                                                                                                                                FEATURES
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                                TITLE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 72); Toyloini; Hominidae; Homo. 1 (bases I to 72); Toyloini, S. V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Camp, N. J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnhan, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Laity, K.E., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M., and Cannon-Albright, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submission
Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt
Lake City, UT 64108, USA
Location/Qualifiers
1.721
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A.,
Tavtigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A.,
Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M.,
Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., K.,
Eavitt, S., Hu, K., Iliev, D., Janecki, T., Kort, E.N., Laity, K.E.,
Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B.,
Peterson, K.T., Raid, J.E., Richards, S., Schroeder, M., Smith, R.,
Snyder, S.C., Swellund, B., Swensen, J., Thomas, A., Tranchant, M.,
and Cannon-Albright, L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <301. .>420
Product—"putative prostate cancer susceptibility protein HPG2/ELAC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="putative prostate cancer susceptibility protein
HPC2/FELAC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="EQRRGKHQPWQSPERPLSRLSPERSSDSESNENEPHLPH"
143 c 184 g 193 t
                                                                                                                                                                                                                                                                                                                                                                  strong candidate prostate cancer susceptibility gene at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAG24439.1"
/db_xref="GI:10880930"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <301. >420
/codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403 AGCCACACTTCCACATGGT 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="17p"
301. .420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AF304371S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-988-687-2 x AF304371S1
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/translation="WMALRSILRPLGLRTMSQGSARRPRPRPRDPRDHHLRTREKRGPGP /translation="WMALRSILRPLGLRTMSQGSARRPRPRPRDPRDHHLRTREKRGPGP /translation="WMALRSILRPLGLRTMSGDGSARRPRPRDPKLKVARLDNIFL TRMHWSDVGGLGMLTLKETGERCVCVELWGEBVQLRTMSPRGESVGRANGEHKLKVARLDNIFL TRMHWSDVGGLGMLTLTKETGERCAPPE SAPEYKYVOVPIHRSRRCGKODSOSPRTSPNRLSPRGOSSDGSABNGCPPE SABGNRKAWGRDPSLVVAFVCKLHLRKGNFLVLKAKELGLPVGTAAIAPIIAAVKD GKSTTYSTGREIAARBELCTPPPDGLUFTUNGEDGSTLDTCUNGTKRYQARADARVA LVVHIAPESVLIDERYQQWMRERFGPOTGLIFTUNGENTSRYQCABADARVA LVVHIAPESVLIDERYQQWMRERFGPOTGLLKYQLRPKREWQROTTLDCNTDEFIABALELP SPOESVEEYKRNOBNPAPARRSOYPEIJFGTGSAIPWINTSRKIOTGLNILLORENDENSY LLDCGGGTGGQLCRRYGQQIPRVLCSLLAYVSHLANDHHTGLLNILLOREHALASLG KPFQPLLVVAPTQLGAMLQOXHNHCQPEILHYSMIPAKCLQKGABVSNTTLERLISLL LETCDLEEFQTCLVRHCKHAFGCALVHSSGWKVVXSGDTMPCGALVQMGKDATLLIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LETCOLLEEGYCLVRHCKHAFGCALVHSSGWKVVYSGDTMPCEALVONGKDATLLIHE
ATLEDGLEEEAVEKTHSTTSGAINVOMRMNAETIMLNHFSQRYAKIPLFSDPBNEKVG
TAFDHMKVCFGOFPTYPKLIPPLKALFAGDIEEMVERREKRELRLVRAALLTQQADSP
EDREPQOKRAHTPSGSKKESVNTLGARV"

8030 c 8142 g 9780 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative prostate cancer susceptibility protein"
/protein_id="AAK29420.1"
/db_xref="GI:13540342"
susceptibility protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 26
Gaps: 0
Percent Identity: 100.000
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       cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS SPAC1D4 31201 bp DNA
DEFINITION S.pombe chromosome I cosmid c1D4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29150 GGAAGGAAGCAGTAGAAAGACACAC 29177
                                                                        /db_xref="GI:13540343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693 uGluGluGluAlaValGluLysThrHis 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="25 exon form"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26.00
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Percent Similarity: 100.000
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US-09-988-687-2 x AF348157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pl:SPAC1D4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E 2 (Dases 1 to 34593)

S Frank, D.C., Swedlund, B., Dumont, M., Tavtiglan, S.V., Simard, J., Tenk, D.C., Swedlund, B., Dumont, M., Tavtiglan, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Frye, C., Chaffari, S., Guyte, J.S., Hu, R., Iliev, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Moorrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swensen, J., Thomas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A. Hows, M. Labrie, E., B. Stopper, C. S. Stopper, C. S. Stopper, C. S. Stopper, C. S. Stopper, S. C. St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putalive prostate cancer susceptibility protein" join(6470. 8650,9077. 9127,9266. 9336,9948. 10012, 1057. 11014,12096. 12164,12933. 13064,14992. 14960, 16609. 16667,16746. 16818,17370. 17482,18671. 18766, 21539. 21677,21757. 21842,23553. 23671,24619. 24715, 22913. 24429,27763. 27801,27930. 28039,28553. 28652, 28733. 28853,29101. 29179,29710. 29854,30406. 30624,
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/note-"putative prostate cancer susceptibility protein"
/groen-"putative prostate cancer susceptibility protein"
/gene-"plac2"
join(8470. .8690,9077. .9127,9266. .9336,9948. .10012,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"

join(<8470. 8690,9077. 9127,9266. 9336,9948. 10012,

join(<8470. 8690,9077. 9127,9266. 9336,9948. 10012,

10057. 11014,12096. 122144,12933. 13064,14902. 14960,

16609. 16667,16746. 16818,17370. 17482,18671. 18766,

21539. 21677,21757. 21842,23553. 23671,24619. 24715,

27291. 27429,27763. 27801,27930. 28039,28553. 28652,

28739. 28853,29101. 29179,29710. 29854,30406. >30639,

//note="alternatively spliced 24 exon form"
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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10957. 11014,12096. 12164,12933. 13064,14902. 14960,
16609. 16667,16746. 16818,17370. 17482,18671. 18766,
21539. 21677, 21757. 21842,22553. 23671,24619. 24715,
27291. 27429,27763. 27801,27930. 28039,28553. 28652,
28733. 28853,29101. 29179,29710. 29854,30406. 30639)
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                                                                                                                                     Mus musculus putative prostate cancer susceptibility protein (Elac2) gene, complete cds, alternatively spliced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="24 exon form"
/codon_start=1
                                                                                                                                                                                                                                                                                          AF348157.1 GI:13540341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"Elac2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="Elac2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .34593
                                                                                                       Mus musculus
                                  seq_name: gb_ro:AF348157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (sites)
                                                                                                                                                                                                                                                                                                                                                    house
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                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                               DEFINITION
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                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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/product="putative golgi peripheral membrane protein"
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/translation="PAFGGIKNFIKEKSEALAGIHRESDESCGFRVLKVENDSKAYNAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STESNVIVVLSKNPLYLVGVSPSTTLSAAYLLSELNLLYCQILTGVTAKAMQLTLNSR
PNFDLRKLIGSNEQFLKELCDQLNDYELVPTLNAISPLPR.SSFRDGLSQLLRETPR
SLLFFTAIRGRLVCMYKAKKLLLHANDLYLLEFLSLFRTGSNBSMEHWVPVCFPTLN
PDAYISTRGFLYCMYKAKKSSESFFEMGSVKCKVAGELQDHGWLKKLIYCEEMD
RTTPRNYGSPCISHLTLFYKKSSESFFFEMGSVKCKVAGELQDHGWLKKLIYCEEMD
RTTPRNYGSPCISHLLLFYKKYSPFKKYSFFFPNPRYFRTJYAILHDQAFHKKN
SFSINMTVHESLLLFTWSTASFPFHCIANATTSSQLLIANVNKILRMIRREENRLFIO
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MDKILQSNSSGDIVVTNDGATILKSIALDNAAAKVLVNISKVQDDEVGDGTTSVCVFA
AELLRQAEIMVNAKIHPQVIIDGYRIATKTAIDALRASSIDNSSDPAKFRSDLENIAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IGMVLQWASIAPAVDAIWHILNVIDDSPVARASLVPYEDYIVGTPEGMMTGEKALSDL
IESHLNRPLRLYIYNHYRDSTRQVTIVPNRHWGGNGAIGCGVGHGVLHRLPAPLSGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQPGDIVFSNPMLGGPDHKVSQPSETENFLPTPEPPKIASANAGSSNEISIPHYQRHK
KSHKGAIQDSSIQSYLDEEEKLSRELDHKTKDASSTNDSQTTPLPPPPPVAVNSTNDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MEPTSEHSSIKEEVENDNVHRSHESECGSLLLNPGNVLMAAPSV
SEDDQEVSRSTPELRSHVENVEQLLSDILHDNSSPLNVSTSVSSSSNNTAVDEIIKLL
                                                                               /note="SPAC1D4.02c, len:345, SIMILARITY:Rattus norvegicus, 035254, golgi peripheral membrane protein p65., (451 aa), fasta scores: opt: 493, E():4.7e-20, (34.4% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="splice branch and acceptor sequence, ctaacgactacag" complement(1964. .1969)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLISFDLAKQKRTYLIFSSSGKPVFSNIVDDSIEPSTVGALQAIISSFEVSKEELTSF
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/note="SPACID4.03c"
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/note="SPACID4.03c"
/gene="Spacida"
/g
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complement(2091. 2108)
/note="ctaaagtgtttttcacag, splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="probable t-complex protein 1, beta subunit"
/protein_id="CAA93213.1"
/db_xref="GI:1177337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="splice branch and acceptor sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(2821. .2836)
/note="splice branch and acceptor sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ctaactafftttta g"
complement(2901. .2906)
forbe="splice donor sequence, gtacgt"
join 5400. .5402.5439. .5570,5618. .7066)
/gene="SPACID4.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="gtatga, splice donor sequence"
complement(join(2574. .2820,2907. .4201))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(5400. .5402,5439. .5570,5618. .7066)
/gene="SPAC1D4.04"
/note="SPAC1D4.04, len:527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1680. .1685)
/note="splice donor sequence, gtatgt"
complement(1874. .1886)
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/protein_id="CAA93212.1"
/db_xref="G1:1177336"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SWISS-PROT:Q10147"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="SWISS-PROT:Q10150"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1637. .1651)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ,2136)
                                                                                                                                                                                                                                                           /codon_start=1
/label=SPAC1D4.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=SPAC1D4.03c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ctaacaatttaacag"
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                                                                                                                                                                                                                       aa)
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                                                                               byrl; cct2; CDP-alcohol phosphatidyltransferase; chaperonin; conjugation and sporulation; cskl; cyclin suppressing protein kinase; DNA repair helicase; golgi peripheral membrane protein; protein kinase; radl5; rhp3; serine threonine protein kinase; stel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing project, Sanger Centre, Hinxton Hall, Hinxton, Cambridge CB10 1RQ E-mail: barrell@sanger.ac.uk Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               URL, http://www.sanger.ac.uk/Projects/S_pombe)
Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in PomBase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program Sp3splice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical 33.0 kd protein"
/Protein_id="CAB56125.1"
/db_xref="GI:5912524"
/translation="mKQIFGTCTGYMNGIYFQEGLLEIPTTKSIRMNSIHIKKKSNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRRRKVFGNEKEFDLEELDDNDIRLRQALEATKRRKIRNSIIGINAEKLLNQETKKEK
OLNTANEPHEANDQTSAQSSKLIEAQLPTVEDRFAKQTNEVDINTHLLNFVEKKLKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLAONY SENGETNALNTKNESTVONIKNSLHPNEHSFIRDAAALGAIREVDLGIISTD
VDNLKNGRKRQKKRARMKEKLDSKALRTSEDAARDEFIEKMLKPISQDEESKGIYRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 31201)
Lye,G., Churcher,C.M., Barrell,B.G., Rajandream,M.A. and Walsh,S.V.
Direct Submission
Submitted (01-FEB-1995) Schizosaccharomyces pombe chromosome I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SP (S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS are numbered using the following system eg SPAC5H10.01c. SP (S CDS) are numbered using the following system eg SPAC5H10.01c. SP (S COMPLementary strand).

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

IMPORTANT: This sequence MAX NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

COSMIG C12H3 and at the 5' end by cosmid c1F3 and at the 3' end by cosmid c12F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this region is derived from cosmid c1D4 is at position 134, while the position 4137 in this sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Details of yeast sequencing at the Sanger Centre are available on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      number of introns/exons or we may not have chosen the correct splice donor/acceptor sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2137. .2316))
/qene="SPACID4.02c"
complement(join(1088. .1636,1686. .1873,1970. .2090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(1088. .1636,1686. .1873,1970. .2090,
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales; Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CP1 beta subunit homologue; tf2 LTR.
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/note="SPAC1D4.01, len:285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="the sequence of c 1F3, the true end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               true end of c1F3 is at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="cosmid c1D4"
/map="IL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/note="SPAC1D4.01"
                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces pombe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                  fission yeast
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AUTHORS
TITLE
JOURNAL
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ACCESSION
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                                                                                   KEYWORDS
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                                            VERSION
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Eakin, N.Q., Morrison, H.G., McArthur, A.G., Nixon, J., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.

Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.

Direct Submitted (07-ARR-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA

* NOTE: This record contains 1 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC031419 938 bp DNA HTG 02-APR-2000 Giardia intestinalis clone EI1687 strain WB-CG, LOW-PASS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glardia intestinalis.
Glardia intestinalis.
Glardia intestinalis
Eukaryota: Diplomonadida; Hexamitidae; Glardiinae; Glardia.
1 (bases 1 to 938)
Morrison, H.G., McAtthur, A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.
Glardia: a model for ancient eukaryotic genome analysis
                                                                                                                                                                  Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia. 1 (bases 1 to 881)
Morfison, H.G., McArthr.A.G., Nixon, J., Eakin, N.Q., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L. Giardia: a model for ancient eukaryotic genome analysis
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Eakin, N.Q., Morrison, H.G., McArthur, A.G., Nixon, J., Kim, U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         881: contig of 881 bp in length
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="EJ0814"
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AC031419.1 GI:7386746
HTG; HTGS_PHASE0.
                                    GI:7524276
                                                                                                   Giardia intestinalis.
Giardia intestinalis
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Percent Similarity: 100.000
                                                                  HTG; HTGS_PHASE0
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US-09-988-687-2 x AC036490
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                             TIGVNCPKVMENANILIANTAMDTDKVKVFGARVRVDTTGKLAELERAEREKMKAKVE
KIKSHNINCFINROLIYNWPEQLFADAGIMSIEHADFDGIERLSLVTGGEIASTFDHP
ELVKLGHCKKIEEIIIGEDKMIKFSGVEAGEACTIVLRGATHQLLDESERAIHDALAV
                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Match to PF00118 cpn60_TCP1, TCP-1/cpn60 chaperonin family Score 590.77"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/label=Spacin4.05c
/product="hypothetical protein"
/product="hypothetical protein"
/protein_id="casa3214.1"
/db_xref="G1:1177338"
/db_xref="G1:1177338"
/translation="MDLEVVEPLHHKLALPFRIGLLVIVGTWLMSVCYHLIYILNRY
OPISPNRRGSLNSRWHHLLQIPLSNRHTDLERWTEFRANLVSPVDFRAGYCFAAILSI
SWATGFILFLKKTQGDIGGLYSHPIYPLLMVITAFILIVFPFPWRYRSSQRGLRKSII
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FFVPLAMAYPFIVAILQCLHYGLSRRKHTFKINLLSALKHATALPVIYLSAIIHAKQT
KFTLTSGHGYLFWLWILSALLSSAYTFLWDVFIDWRIRFPFHKSINHKRFPWFIYAIG
                                                                                                                                 LSQTVAESRVTLGGGCAEMLMAKAVEEAATHEPGKKAVAVSAFAKALSQLPTILADNA
GFDSSELVAQLKAAHYDGNDTWGLDMDEGEIADMRAKGILEALKLKQAVVSSGSEGAQ
LLLRVDTILKAAPRPRERM"
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fasta scores: opt: 261, E():1.5e-10, (25.1% identity in
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/gene="SPACID4.05c"
/note="SPACID4.05c"
/not
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LOCUS AC036490 881 bp DNA HTG 07-APR-2000
DEFINITION Giardia intestinalis clone EJ0814 strain WB-C6, LOW-FASS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPACID4.05c, len:387, SIMILARITY:Mus musculus, Q9Z0U0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttaacgatttatag"
5741. 5767
/gene="SPACID4.04"
/note="PSPACID4.04"
/gene="SPACID4.05c"
                                                                                                                                                                                                                                            5425. .5438
/note="splice branch and acceptor sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="splice branch and acceptor sequence
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join(5529. .5570,5618. .7045)
/gene="SPAC1D4.04"
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Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L.
Direct Submission
L Submitted (02-APR-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
* NOTE: This record contains 1 individual
* Sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* Will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Furbidopsis thaliana
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots:
Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 46335)
Lin,X., Kauli,S., Tomn,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome 1 BAC F915 genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-OCT-2000) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org Address all correspondence to:at@tigr.org
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Arabidopsis thaliana chromosome 1 BAC F915 genomic sequence,
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Gaps: 0
Percent Identity: 100.000
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/organism="Giardia intestinalis"
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/clone="E11687"
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Genes were identified by a combination of several methods: Gene prediction programs including Genesan+ (Chris Burge, http://ccr.081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerA, see Mihaela Pertea, Http://www.tigr.org/softlab/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TiGR (http://www.tigr.org/tdb/tgl.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein profession proteins over most of their length are annotated as similarity are named as unknown proteins. Genes without protein professions. Genes encoding tRNAs are predicted by transcrible tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ttp.genome.washington.edu/RW/Repeatmasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/protein_id="AAG260II.1"
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NPTNTIAYAQILGTGMDTQDTSSSVLLFFDKQRFIFNAGEGLQRFCTEHKIKLSKIDH
VFLSRVCSETAGGLPGLLLTLAGIGEEGLSVNVWGPSDLNYLVDAMKSFIPRAAMVHT
clone F915 is from Arabidopsis thaliana chromosome 1 orientation of the sequence is from SP6 to 77 end of the BAC \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9016,
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10177. .10221,10306. .10395,10478. .10639))
/gene="F915.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to HD-zip (Arabidopsis thaliana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Arabidopsis thaliana"/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="unknown protein"
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'Ypt_family="(GAGAA)n"

complement(1169. .1195)

/rpt_family="AT_rich"

complement(1562. .1608)

/rpt_family="AT_rich"

complement(2125. .154)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(<126. .>334)
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complement(3622. .3728)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="F915.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="F915"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:1149569"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .46335
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complement(26608. .26641)
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complement(27450. .27491)
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complement(join(<28479. .28732, 29099. .29311, 29402. .29473, 29582. .>29780)
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GPLVDQVRNGRVNGVREEEELIDIVGKGFEKEDLSPVVKTN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 46335
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Gaps: 0
Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="unknown protein"
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                                                                           .21990)
                                                                                                                                                                                                                                                                                                                                                        complement(28479. .29780)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:10998866"
                                                                        complement(21969. .219
/rpt_family="AT_rich"
complement(26156. .261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to reverse of: AC022354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="tRNA-Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                           29582. .29780))
/gene="F915.19"
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US-09-988-687-2 x AC022354/rev
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Ratio: 1.000
Percent Similarity: 100.000
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complement(20931. .20985)
/rpt_family="(GAA)n"
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/gene="F915.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Arabidopsis thallana (Mouse-ear cress))"
join(21044. 21140,21233. .21450,23180. .23739,24098. .25046)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MAVDEVSIFIGVASLTVSVWWFINKFTVLEAVPTSNAIPIHSVA
VRVGSTQRVVWEIIITFALVYTVXATAIDSNNGTLGTTAPLAIRLIVGANILAAGPFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MENPPNETEAKQIQTNEGKKTKGGIITMPFIIANEAFEKVASYG
LLPNMIMYLIRDYRFGVAKGTNVLFWMSAASNFTPLLGAFLSDSYLGRFLTISIASLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLGMVLLMLTAMLPQVKPSPCDPTAAGSHCGSSTASQLALLYSAFALISIGSGGIRP
CSLAFGADQLDNKENPKNERVLESFFGWYYASSAVAVLIAFTGIYYIQEHLGWKIGFG
VPAVLMLIAALLFILASPLYVTRGVTKSLFTGLAQAIVAAYKKRKLSLPDHHDSFDCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPIWSTGIMMSINTSQSSFQLLQATSMDRRLSRHGSSFQVPAGSFGMFTIIALALWVI
LYDRAVIPLASKIRGRPFRLSVKLRMGLGLFWSFLAMAISAMVESFRRKKAISOGYAN
NSNAVVDISAMWLVPQYVLHGLAEALTAIGQTEFFYTEFPKSMSSIAASLFGLGMAVA
                        DLEKAKKVFGVKPGPKYSRLQSGESVKSDERDITVHPSDVMGPSLPGPIVLLVDCPTE
SHAAELFSLKSLESYYSSPDEQTIGAKFVNCIIHLSPSSVTSSPTYQSWMKKFHLTQH
ILAGHQRFLPLLIIVSHQKTVRKNMAFPILKASSRIAARLNYLCPQFFPAPGFWPSQL
                                                                                                TDNSIIDPTPSNKFNLRPVAIRGIDRSCIPAPLTSSEVVDELLSEIPEIKDKSEEIKO
FWNKQHNKTIIEKLWLSECNTVLPNCLEKIRRDDMEIVILGTGSSQPSKYRNVSAIFI
DLFSRGSLLLDCGEGTLGQLKRRYGLDGADEAVRKLRCIWISHIHADHHTGLARILAL
                                                                                                                                                                                                       EGSLETQGSPMQSVFRRSDISMDNSSVLLCLKNLKKVLSEIGLNDLISFPVVHCPQAY
GVVIRAAERVNSVGEQLIGMKMYYSDSDRPCPETVEASBATILIHEAFFEDALLEEA
LAKHHSTTKEALDVGSAANVYRIVLHFSQRYPKIPVIDESHHHNTCIAFDLMSINMA
DLHVLPKVLPYFKTLFRDEMVEDEDADDVAMDDLKEEAL"
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RSFGPSSTPDPIVLVNDEVVKISAIILKPCHSEEDSGNKSGDLSVVYVCELPEILGKF
                                                                                                                                                                              RSKLLKGVTHEPVIVVGPRPLKRFLDAYQRLEDLDMEFLDCRSTTATSWASLESGGEA
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                                                                                                                                                                                                                                                                                                     complement(join(<11317. .11583,12194. .>12301))
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/gene="F915.3"
/note="similar to delta tonoplast integral protein
GI:1145697 (Arabidopsis thaliana)"
/complement(join(11317. .11583,12194. .12301))
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/protein_id="AAF29404.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"aquaporin, putative"
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/rpt_family="AT_rich"
complement(16191. .16271)
/rpt_family="AT_rich"
complement(17443. .17472)
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complement(1841. .18182)
/rpt_family="AT_rich"
/rpt_family="AT_rich"
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/rpt_family="AT_rich"
/rpt_family="AT_rich"
/rpt_family="AT_rich"
/rpt_family="AT_rich"
/rpt_family="AT_rich"
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19668. .19760
/rpt_family="(A)n"
complement(20768. .20803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGPMNPGRSFGSSLAVGNFSGH"
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TYPE: PRT ORGANISM: Saccharomyces cerevisiae
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les 9; Conser'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              682 LLIHEATLE 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         717 LLIHEATLE 725
US-09-315-794-52
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US-09-389-341-52
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-315-794-52
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LENGTH: 838
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 838
                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                 (without alignments)
1310.841 Million cell updates/sec
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Sequence 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                  1 MWALCSLLRSAAGRTMSQGR.....EPQQKRAHTEEPQAKKVRAQ
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                                                                      Search time 14.18 Seconds
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-878-989-7
US-08-878-989-7
US-08-677-049-8
US-08-677-049-10
US-08-320-559-31
US-08-345-860D-31
PCT-US94-04496-31
US-08-451-715A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-981-392-33
US-08-685-992-7
US-09-144-925-7
US-08-036-210-13
US-08-449-609-13
                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT-US93-01901-17
US-08-595-043A-73
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US-08-348-353-17
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                                                                                                                                                                                      212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                     March 29, 2002, 10:20:53;
                                                                                                                                                                                                                                                                                     Post-processing: Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                  Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                          Issued_Patents_AA:*
                                                                                                                                                                                                                                                     seq length: 0
seq length: 2000000000
                                                                                                                US-09-988-687-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match Length DB
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1248
1248
1248
1261
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                                                                                                                         Perfect score:
                                                                                                                                                        Scoring table:
                                                 OM protein
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Maximum DB
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                                                                                                                                                                                       Searched:
                                                                                                                                     Sequence:
                                                                      Run on:
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215, App
40, Appl
2, Appl
16, Appl
16, Appl
16, Appl
16, Appl
16, Appl
182, Appl
182, Appl
182, Appl
181, Appl
11, Appl
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                                                                                                            Sequence Seq
US-08-764-640-40
US-08-973-225-40
US-08-973-225-40
US-09-973-225-215
US-09-516-704-40
PCT-US95-01140-2
US-08-455-655-16
US-08-455-685-16
US-08-455-685-16
US-08-455-685-16
US-08-455-685-16
US-08-455-685-16
US-08-455-63-16
US-08-851-843A-182
US-08-851-843A-182
US-08-851-843A-182
US-08-974-549A-301
US-08-974-549A-301
US-08-974-549A-301
US-08-974-549A-301
US-08-974-050-182
US-08-974-050-182
US-08-140-188-13
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Sequence 52, Application US/09315794

Patent No. 6197517

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 9301-053
CURRENT APPLICATION NUMBER: US/09/315,794
CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Roberts, Christopher J.
TITLE OF INVENTION: ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
TITLE OF INVENTION: AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATIVE
TITLE OF INVENTION: DRUGS.
FILE REPERENCE: 9301-057
CURRENT APPLICATION NUMBER: US/09/389,341
CURRENT PILING DATE: 1999-09-02
EARLIER APPLICATION NUMBER: 09/315,794
EARLIER PILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PALENTIN VOY: 2.0
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100.0%; Pred. No. 2.2
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 52, Application US/09389341; Patent No. 6200803; GENERAL INFORMATION:
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NUCLEOTIDE AND PROTEIN SEQUENCES
OF VERTEBRATE DELTA GENES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tonks, Nicholas
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
STREET: Two Militia Drive
CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 7; DB 4;
100.0%; Pred. No. 14;
iive 0; Mismatches
                 Artavanis-Tsakonas, Spyridon
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Antler, Adriane M.
REGISTRATION NUMBER: 32,605
REFERENCE/DOCKET NUMBER: 7126-038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-90-9090
TELEPAX: 212-86-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                         ZIP: 10.036/2711
ZIP: 10.036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESSESO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,392
FILING DATE: Z2-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                         NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/685,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08685992
Patent No. 5912138
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.8
Best Local Similarity 100.
Matches 7; Conservative
               APPLICANT: Artavanis-Ts
APPLICANT: Gray, Grace
TITLE OF INVENTION: NUC
TITLE OF INVENTION: OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-981-392-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 PLSRLSP 209
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TOPOLOGY: un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: USA
ZIP: 02173
                                                                                                                                                                                             X
                                                                                                                                                                                           STATE: N
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-685-992-7
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                                                                                                                                                                                                                                                                                                                          APPLICANT: GREENLAND, Andrew James
APPLICANT: DRAPER, John
APPLICANT: SKIPSEY, Manc
APPLICANT: WARNER, Simon
APPLICANT: WARNER, Simon
TITLE OF INVENTION: S-ADENOSYL-L-HOMOCKSTEIN HYDROLASE PROMOTER
CORRESPONDENCES: 10
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                                                   Length 838;
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                                                                                               0; Indels
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                                           1.1%; >cc.
100.0%; Pred. No. ...
0; Mismatches
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Patent No. 6262025
GENERAL INFORMATION:
APPLICANT: Ish-Horowicz, David
APPLICANT: Henrique, Domingos Manuel Pinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Pred. No. 4.4
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/00882
FILING DATE: 10-APPL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9507381.3
FILING DATE: 10-APR-1995
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pillsbury Madison & Sutro STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.0%; Score 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: U.S.A.
ZIP. 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/930,894
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: TOBACCO SHH PROTEIN
                                                                                                                                                                                                                                               US-08-930-894-5; Sequence 5, Application US/08930894; Sequence No. 6037524; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 138 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: MS Word
CURRENT APPLICATION DATA:
                                                                                             9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                       717 LLIHEATLE 725
                                                                                                                                 682 LLIHEATLE 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-08-981-392-33
US-09-389-341-52
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Length 289;
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                                                                                                                         Length 250;
                                                                                                                                                                                                                                                                                                                                        Sequence 13, Application US/08036210
Patent No. 5585233
GENERAL INFORMATION:
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ulirich, Axain B.
TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE TITLE OF INVENTION: PTP-S31: A NOVEL PROTEIN TYROSINE NUMBER OF SEQUENCES: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/08/036,210
FILING DATE: 23-MR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
5. 88;
                                                                                                              0.8%; 5cc.
100.0%; Pred. No.
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 1155 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 13, Application US/08449609
; Patent No. 5952212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTATION NUMBER: 18,825
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.8%; Soc
Best Local Similarity 100.0%; Pi
Matches 7; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                          ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-036-210-13
        STRANDEDNESS: single
                          ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-144-925-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                       783 EKRELRQ 789
                                                                                                                                                                                                                                |||||||
137 EKRELRQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       783 EKRELRQ 789
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| 177 EKRELRQ 183
                                                                                                                                                                                                                                                                                                          RESULT 7
US-08-036-210-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-449-609-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09144925
Patent No. 5951979
GENERAL INFORMATION:
APPLICANT: TONKS, NICHOLAS
APPLICANT: Flint, Andrew J.
TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 07421-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 7; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Pred. ...
FILING DATE: 25-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03
TELECHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTURNEY, CALLER AND TATTICIA
NAME: Grandhan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL96-03Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/685,992
FILING DATE: July 25, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: HAMILTON, BROOK
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: 1.ENGTH: 250 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.8
Best Local Similarity 100.
Matches 7; Conservative
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TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1111111
137 EKRELRQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                783 EKRELRQ 789
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Patent No. 6207148
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: COTIEY, Neil C.
APPLICANT: COTIEY, Neil C.
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENTING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
FILLING DATE: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.8%; Score 7; DB 2
100.0%; Pred. No. 99;
live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                FILLNG DATE:
ATTORNEY/AGENT INFORMATION:
NAME: B111ngs, Lucy J J RECISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECHONICATION INFORMATION:
TELECHONE: 415-855-0555
TELECHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH 328 amino acids
TYPE: amino acid
STRANDENESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.8
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PENITUT01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LIBRARY: PENITU; CLONE: 1452972
US-08-878-989-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503 LVNISPD 509
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ZIP: 94304
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-272-796-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
              APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
APPLICANT: Ullitch, Axel
TITLE OF INVENTION: PPP-531: A NOVEL PROTEIN TYROSINE
TITLE OF INVENTION: PHOSPHATASE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                               SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,609
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION WHERE: 23-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. LEGILE
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 7683-025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08878989;
Patent No. 5885803;
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Guegler, Karl G.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 7; DB 2
100.0%; Pred. No. 88;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                      ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8664/9741
TELEX: 66141 PENNE;
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                   New York
                                                                                                                                                                                                               STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Palo Alto
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  783 EKRELRQ 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-449-609-13
                                                                                                                                                                           STREET:
CITY: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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STATE:
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Sequence 10, Application US/08677049

Patent No. 5858707

GENERAL INFORMATION:

APPLICANT: Guinaraes, M. Jorge

APPLICANT: Acclanahan, Terrill K.

APPLICANT: Lalorik, Albert

APPLICANT: Lalorik, Albert

TITLE OF INVENTION: NUCLEIC ACIDS; ANTIBODIES

NUMBER OF SEQUENCES: 12

CORRESPONDENCE SS:

ADDRESSE: DANX Research Institute

STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Region
LOCATION: 363..390
OTHER INFORMATION: /note- "Encompasses TM 10 of Figure
US-08-677-049-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.8%; Score 7; DB 2; Length 432;
100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                             /note= "Encompasses TM 4 of Figure
                                                                                                                                                                                                                                                                                     /note= "Encompasses TM 9 of Figure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDTIN TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,049
FILING DATE: 03-JUL-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,788
FILING DATE: 03-JUL-1996
ATTONEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: DX0511
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 415-496-1200 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 460 amino acids
      432 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.8
Best Local Similarity 100.
Matches 7; Conservative
                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                       MOLECULE TYPE: protein FEATURE:
                                                                                                                              NAME/KEY: Region
LOCATION: 115..144
OTHER INFORMATION: 4
FEATURE: Region
LOCATION: 325..359
OTHER INFORMATION: 7
OTHER INFORMATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 IAPIIAA 277
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US-08-677-049-10
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APPLICANT: Bazan, J. Fernando
APPLICANT: Bazan, J. Fernando
APPLICANT: Bazan, J. Fernando
APPLICANT: ALOCAIA Albert
TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEOBASE PERMEASES;
TITLE OF INVENTION: NUCLEIC ACIDS; ANTIBODIES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: DANA Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/677,049 FILING DATE: 03-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 03-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,788
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08677049 Patent No. 5858707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090 REFERENCE/DOCKET NUMBER: DXC TELECOMMUNICATION INFORMATION: TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.8%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415-496-1200
                                                                                                                                                                                                                 TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                : PENITUT01
1452972
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PENITU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Sequence 31, Application US/08545860D
Patent No. 6040140
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canani, Ell
APPLICANT: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.8%; Score 7; DB 1; Length 559; 100.0%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz & ADDRESSEE: No. 6040140ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFTWALES PATENTING SISTEMS

CORRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-MAR-1996
CLASSIFICATION A35
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994
PRIOR APPLICATION DATE: 22-APR-1994
PRIOR APPLICATION NUMBER: PCT/US92/10930
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                   RECEINATION NOTHERS.
REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
TELEFURN: (215) 568-3439
TELEFAX: (215) 568-3439
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
NOLECULE TYPE: protein
US-08-320-559-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 14-MAY-1993
PRIOR APPLICATION NUMBER: US 07/97' ...
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JMBER: US 07/888,839
27-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   REGISTRATION NUMBER: 33,229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.8°
Best Local Similarity 100°
Matches 7; Conservative
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COMPUTER READABLE FORM:
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202 RERPRKD 208
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US-08-545-860D-31
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Patent No. 5633135
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                             0.8%; Score 7; DB 2; Length 460; 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
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APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRICE APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-007-92
PRICE APPLICATION DATA:
APPLICATION NUMBER: US/07/808,830
FILING DATE: 27-MAY-92
PRICE APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
NAME: DELUCA, MARK
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.8 Best Local Similarity 100. Matches 7; Conservative
                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                            MOLECULE TYPE: protein FEATURE:
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amino acid
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US-08-320-559-31
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GENERAL INFORMATION:
APPLICANT: Canaani, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: For Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewitz &
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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O.8%; Score 7; DB 3; Length 559;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERTING SYSTEM: PC-DGS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: PCT/US94/04496
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca ESQ., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: 7JU-1262
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (215) 568-3100
TELEFRAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 559 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: protein
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NAME: DeLuca Esq., Mark
REGISTATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEPHONE: (215) 568-3439
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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PCT-US94-04496-31
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Query Match

0.8%; Score 7; DB 5; Length 559;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy 29 RERPRKD 35
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Search completed: March 29, 2002, 10:23:12 Job time: 139 sec

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(without alignments)
3762.720 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                               OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Q21169 caenorhabdi
086707 streptomyce
0990u5 pyrococcus
059139 pyrococcus
058883 pyrococcus
05881 pyrococcus
059601 allium cepa
091x59 homo sapien
031x65 arthrobacte
091x26 trypanosoma
041x93 nicotiana s
04239 nicotiana s
04539 licotiana s
04539 licotiana s
04539 licotiana s
04544 clostridium
059wf5 lycopersico
091k36 arabidopsis
091x6 arabidopsis
091x0 arabidopsis
091x0 arabidopsis
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091x0 arabidopsis
091x0 pseudomonas
094x48 homo sapien
090x18 coccidicide
050125 mycobacteri
060125 mycobacteri

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_invertebrate:*
sp_mammal:*
sp_mhc:*

sp_organelle:* sp_phage:*

4: 5:: 6:: 7:: 10: 11: 12: 14:

sp_plant:* sp_rodent:*

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*

SPTREMBL_17:*

Database

Result Ouery No. Score Match Length DB ID Description 2 725 87.8 826 4 09HaS8 09bq52 homo sapien 09hrs homo sapien 09hrs

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ALIGNMENTS	PRESULT 1 09HAS8 DD 09HAS8: CD 09HAS8: DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DC 01-MAR-2001 (TrEMBLRel. 16, Last sequence u	2ue Bes Mat	UY IMMALCSLIKSAAGKTINSQCRTISQARAKEKKINDEJAHLKITAKROSGCSGCSGCSGCSGCTNIYIL OU IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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Homo sapiens (Human)
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LSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKGIELAVRPHSAPEYEDETMTV
                                  VAFICKLHLKRGNFLVLKAKEMGLPVGTAAIAPIIAAVKDGKSITHEGREILAEELCTPP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE PROSTATE CANCER SUSCEPTIBILITY PROTEIN.
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TISSUE-LUNG CARCINOMA;
Strausberg R.,
Submitted (JAN-2001) to the EM
EMBL; BC004158; AAH04158.1; -.
EMBL; BC001939; AAH01939.1; -.
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TISSUE-LUNG CARCINOMA;
Strausberg R.;
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CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CDNA FLJ10530 FIS, CLONE NT2RP2000985.
8B3A38C355757AAE
                                    Score 725; DB
Pred. No. 0;
0; Mismatches
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MW;
                                    87.8%;
99.9%;
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AA;
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es 825; Conserv
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Query Match
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Q9GL73;
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09GL72
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                                                                                                                                                                                                                                                                   61 QVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKVARLDNIFLTRMHWSNVGG 120
                                                                                                                                                                                                                                                                              121 LSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKGIELAVRPHSAPEYEDETMTV 180
                                                                                                                                                                                                                                                                                                                    YQIPIHSEQRRGKHQPWQSPERPLSRLSPERSSDSESNENEPHLPHGVSQRRGVRDSSLV 240
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                                                                                                                                                                                                                           1 MWALCSLLRSAAGRIMSQGRIISQAPARRERPRKDPLRHLRIREKRGPSGCSGGPNIVYL 60
                                              Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M. Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Niboniya K., Iwayannafi T.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 VAFICKLHLKRGNFLVLKAKEMGLPVGTAAIAPIIAAVKDGKSITHEGREILAEELCTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HISMIPAKCLQEGAEISSPAVERLISSLLRTCDLEEFQTCLVRHCKHAFGCALVHTSGWK
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                                                                                                                                                                                                                                                                                                                                                           CLLKYQLRPRREWQRDAIITCNPEEFIVEALQLPNFQQSVQEYRRSAQDGPAPAEKRSQY
                                                                                                                                                                                                       ;
                                                                                                                                                                                  Length 854;
                                                                                                                                                                                                       Indels
                                                                                                                                                     95138 MW; DF9F32846C7166B1 CRC64;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                       ;
                                                                                                                                                                                  52.1%; Score 430; DB 4; 99.6%; Pred. No. 0;
                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                             Pred. No.
                                                                                                                                                                                                      Matches 750; Conservative
                                                                                                                                                      854 AA;
                                                                                                                                                                                             Local Similarity
                                        SEQUENCE FROM N.A.
                      NCBI_TaxID=9606;
                                                                                                                                                      SEQUENCE
                                                                                                                                                                                  Query Match
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Tavitigian S.V., Simard J., Teng D.H.F., Baumgard M., Beck A.,
Tavitigian S.V., Simard J., Teng D.H.F., Bayananth P., Desrochers M.,
Dumont M., Farnham J.M., Frank D., Frye C., Ghaffari S., Gupte J.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 OREMOEHKLKVARLDNIFLTRMHWSNVGGLSGMILTLKETGLPRCVLSGPPQLEKYLEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 KIFSGPLKGIELAVRPHSAPEYEDETMTVYQIPIHSEQRRGKHQPWQSPERPLSRLSPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 KIFSGPLKGIELAVRPHSAPEYEDETMTVYQIPIHSEQRRGKHQPWQSPERPLSRLSPER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tavtigian S.V., Simard J., Teng D.H.F., Baumgard M., Dayananth P., Tavtigian S.V., Simard J., Farnham J.M., Frank D., Frye C., Ghaffari S., Gupte J.S., Hu R., Iliev D., Janecki T., Kort E.N., Laity K., Leavitt A., Leblanc G., McArthur-Morrison J., Pederson K.T., Reid J.E., Richards S., Schroeder M., Smith R., Snyder S.C., Swedlund B., Swensen J., Thomas A., Tranchant M., Woodland A.-M., Labrie F., Skolnick M.H., Neuhausen Kommens J., Cannon-Albright L.A.; "Pan troglodytes ortholog of human HPC2/ELAC2."; Submitted (SEP-2000) to the EMBL, AF308698, AAG24220.1; "Pan Embl. AAG24220.1; "Pan
                                                                                                                                                                                                                                                      Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                            Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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    AA.
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826
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                                   Q9GL72;
01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel, 16, 01-MAR-2001 (TrEMBLrel. 16,
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01-MAR-2001 (
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SEQUENCE FROM N.A.

Tavtigian S.V., Simard J., Teng D.H.F., Baumgard M., Beck A.,

Tavtigian S.V., Simard J., Teng D.H.F., Baumgard M., Beck A.,

Camp N.J., Carllo A.R., Chen Y., Dayananth P., Desrochers M.,

Dumont M., Farnham J.M., Frank D., Frye C., Ghaffari S., Gupte J.S.,

Hu R., Iliev D., Janecki T., Kort E.N., Laity K.E., Leavitt A.,

Hu R., Iliev D., Janecki T., Kort E.N., Farl B., Pern B., Peterson K.T.,

Reid J.E., Richards S., Schroeder M., Smith R., Snyder S.C.,

Swedlund B., Swensen J., Thomas A., Tranchant M., Woodland A.-M.,

Cannon-Albright L.A.;

Mouse ortholog of human HPC2/ELAC2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trank D.C. Swedlund B., Dumont M., Tavtigian S.V., Simard J., Trong D.H.F., Baumgard M., Beck A., Camp N.J., Carillo A.R., Chen Y., Dayananth P., Desrochers M., Farnham J.M., Frye C., Glaffari S., Gupte J.S., Hu R., Iliav D., Janecki T., Kort E.N., Laity K.E., Leavitt A., Leblanc G., McArthur-Morrison J., Pederson A., Penn B., Peterson K.T., Reid J.E., Richards S., Schroeder M., Smith R., Snyder S.C., Swensen J., Thomas A., Tranchant M., Woodland A.-M., Labrie F., Skolnick M.H., Neuhausen S., Rommens J.,
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 GMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKGIELAVRPHSAPEY 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mouse Elac2-containing genomic DNA.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF348157; AAK29420.1;
SEQUENCE 831 AA; 92729 WW; F49FCGC65C9FDDEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC_2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF308696; AAG24918.2; --
MGD; MGI:1915876; 1110017007Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         831 AA; 92631 MW; 4EA7DFAC292E2B32 CRC64;
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    Last sequence update)
Last annotation update)
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.2%; Score 51; DB 11;
100.0%; Pred. No. 2.2e-43
Live 0; Mismatches 0
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       16,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.2%
Best Local Similarity 100.0
Matches 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
    01-MAR-2001 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
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Labrie F., Skolnick M
Cannon-Albright L.A.;
                                                                      1110017007RIK.
Mus musculus (Mouse)
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Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Hu R., Iliev D., Janecki T., Kort E.N., Laity K.E., Leavitt A., Leblanc G., McArthur-Morrison J., Pederson A., Penn B., Peterson K.T., Reid J.E., Richards S., Schroeder M., Smith R., Snyder S.C., Swedlund B., Swensen J., Thomas A., Tranchant M., Woodland A.-M., Labrie F., Skolnick M.H., Neuhausen S., Rommens J., Cannon Albright L.A.;
"Gorilla gorilla ortholog of human HPC2/ELAC2.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                        643 RHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATLLIHEATLEDGLEEEAVEKTH 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 RHCKHAFGCALVHTSGWKVVYSGDTMPCEALVRMGKDATLLIHEATLEDGLEEEAVEKTH 702
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                   Length 826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 824;
                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mouse Elac2-containing genomic DNA.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                             826 AA; 92260 MW; D323B5F3D8B294A6 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE PROSTATE CANCER SUSCEPTIBILITY PROTEIN.
                                                                                                                                                                                                                                                                                 19.0%; Score 157; DB 6; Le
100.0%; Pred. No. 4.3e-153;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 STTSQAISVGMRMNAEFIMLNHFSQRYAKVPLFSPNF 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
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01-MAR-2001 (TrEMBLrel. 16, Created)
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                                                                                                                                                                                                                                                                                                         al Similarity 100.
157; Conservative
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Cannon-Albright L.A.;
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01-JUN-2001
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         Query Match
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Q9D1A8;
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Q9D1A8
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE PROSTATE CANCER SUSCEPTIBILITY PROTEIN HPC2/ELAC2 (FRAGMENT).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE PROSTATE CANCER SUSCEPTIBILITY PROTEIN HPC2/ELAC2 (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 4...
                                                                                         46 AA.
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
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                                                                                         PRELIMINARY;
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Les 46; Conserv
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Cannon-Albright
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                                                                                     Q9HAS9
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6
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Matches
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RESULT
Q9HAS9
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DNA SEGMENT, CHR 11, WAYNE STATE UNIVERSITY 80, EXPRESSED (FRAGMENT).
                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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4.7%; Score 39; DB 4; Length 39; 100.0%; Pred. No. 3.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25346 MW; A82E61B36A57DC60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11; L 2.5e-26;
                                                                                                                                               1 EQRRGKHQPWQSPERPLSRLSPERSSDSESNENEPHLPH 39
                                                                                                                 188 EQRRGKHQPWQSPERPLSRLSPERSSDSESNENEPHLPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         676 MGKDATLLIHEATLEDGLEEEAVEKTHSTTSQAI 709
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.1%; Score 34; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AK003759; BAB22981.1; -.
MGD; MGI:1915876; 1110017007Rik.
                       100.0%;
                                                        39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34; Conservative
                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
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1110017007RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
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Best Local Similarity
                             Best Local Similarity
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RECENTED FOR THE PROBLEM OF THE PROB
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F915.1.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                             1.2%; Score 10; DB 10; Length 837; 100.0%; Pred. No. 0.58;
                                                                                                                                                          Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation update)
                                                                                                                                     Last sequence update)
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                                                     837 AA.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAY-2001 (TrEMBLrel. 16, Last ann
CG3298 PROTEIN.
JHI-1 OR CG3298.
                                                                                                          Created)
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                                                                                                     01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100. Matches 10; Conservative
                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
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                                                     Q9M819
Q9M819;
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     RESULT 14
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                                                                                                                  Arakawa T., Shinagawa K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Shinagawa K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Konno H., Adachi J., Fukuda S., Arawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Saito R., Richi P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H., Kohil P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H., Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Askai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Anorone P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sakawi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wynshaw-Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Functional annotation of a full-length mouse cDNA collection.";
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01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
SIMILAR TO SCHIZOSACCHAROMYCES POMBE CHROMOSOME I COSMID C1D4.
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0431F01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.2%; Score 10; DB 10; Length 805; 100.0%; Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 4.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 MGKDATLLIHEATLEDGLEEEAVEKTHSTTSQAI 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             676 MGKDATLLIHEATLEDGLEEEAVEKTHSTTSQAI 709
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01-07-2000 (TrEMBLrel. 15, Last seq
01-07-2000 (TrEMBLrel. 15, Last sem
                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; Pubmed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 409:685-690(2001).
EMBL; AK004136; BAB23185.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:106352; D11Wsu80e.
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Best Local Similarity
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les 10; Conserv
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ehrhartoideae;
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Best Loca

RESULT 13

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09LWQ4

Matches

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Indels

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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Laik C. Lain X.,
RA Lask D., Led Y., Ledvitsky A.A., Li J., Lin X.,
RA Lask D., Led Y., Ledvitsky A.A., Li J., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,
RA Palazzolo M., Pittana G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Sher B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
RA Gibbs R.A., Myers E.W., Rubin G.W., Venter I.,
RA Gibbs R.A., Myers E.W., Rubin G.W., Venter I.,
R. Science 287:2185-2195(2000)
R. Science 287:2185-2195(2000)
R. Sequence C. Tarana M., 704327777345D01D CRC64;

Query Match

Query Match

Query Match

Query Match

Best Local Similarity 100.0%, Pred. No. 5.7;

Db Strucked G.B

RALENCE TAS AA; Best William Secore 9; DB 5; Length 743;

Best Local Similarity 100.0%, Pred. No. 5.7;

Ob Search completed: March 29, 2002, 10:24:21
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P58142 rhizobium 1 P7972 gallus gall P51567 arabhidopsis P48165 homo sapien P41006 bacillus ca 067166 aquifex aeo P28236 mus musculu P55917 ovis aries P54644 dictyostell P39618 bacillus su Q9kru4 vibrio chol Q9kru4 vibrio chol

GPDA_RHILO
FXD3_CHICK
AFC2_ARATH
CXA8_HUMAN
PYRP_BACCL
PROA_AQUAE
CXA8_SHEEP
KRAC_DICDI
WDDJ_BACSU
NORM_VIBCH

3343 444432 444433 44443 4644 4611

8888888888888

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333334 44444 5433334 5433334 5433334

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826
1 MWALCSLLRSAAGRTMSQGR..........EPQQKRAHTEEPQAKKVRAQ 826
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters;
                                                                                                                                                                                                                                                               100059 segs, 36664827 residues
                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                   OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                         US-09-988-687-2
                                                                                                                                                                                                                                                                                                                                                                                                                                          SwissProt_39:*
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                               Searched:
                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|        |       | d     |        |    | SUMMARIES  |                     |
|--------|-------|-------|--------|----|------------|---------------------|
| Result |       | Query |        |    |            |                     |
| NO.    | Score | Match | Length | BB | ΩI         | Description         |
| 1      | 11    | 1.3   | 808    | 7  | YATA_SCHPO | Q10155 schizosacch  |
| 7      | 6     | 1.1   | 838    | ٦  | YK59_YEAST | P36159 saccharomyc  |
| m      | 80    | 1.0   | 423    | ÷  | DCOR_TRYBB | P07805 trypanosoma  |
| 4      | 80    | 1.0   | 485    | 7  | SAHH_ARATH |                     |
| S      | 8     | 1.0   | 485    | 7  | SAHH_CATRO | P35007 catharanthu  |
| 9      | 80    | •     | 485    | П  | SAHH_MESCR | P93253 mesembryant  |
| 7      | 8     | 1.0   | 485    | П  | SAHH_PETCR | Q01781 petroselinu  |
| 80     | 80    | 1.0   | 485    | П  | SAHH_PHASS | P50249 phalaenopsi  |
| 6      | 80    | 1.0   | 485    | Н  | SAHH_TOBAC |                     |
| 10     | 80    |       | 485    | -  | SAHH_WHEAT | P32112 triticum ae  |
| 11     | ∞     |       | 836    | -  | Y167_HUMAN | Q99490 homo sapien  |
| 12     | ω     |       | 1276   | П  | MDR2_CRIGR | P21449 cricetulus . |
| 13     | 7     |       | 71     | _  | YCX4_MESVI | Q9mur2 mesostiqma   |
| 14     | 7     |       | 129    | Н  | IR08_HCMVA | P16806 human cytom  |
| 15     | 7     | 0.8   | 129    | ~  | VG42_HSVI1 |                     |
| 16     | 7     | •     | 211    | ٦  | LEF7_NPVOP | O10362 orgyia pseu  |
| 17     | 7     |       | 216    | Н  | INAA_ECOLI |                     |
| 18     | 7     | ٠     | 220    | ~  | TPIS_CHLAU | P96744 chloroflexu  |
| 19     | 7     |       | 241    | 7  | KORA_STRLI |                     |
| 20     | 7     |       | 258    |    | SN29_HUMAN |                     |
|        | 7     | •     | 259    | -+ | PPNK_MYCPN | P75508 mycoplasma   |
|        | 7     |       | 264    |    | RPOD_ARCFU | O28002 archaeoglob  |
| 23     | 7     |       | 264    | П  | SNAI_MOUSE | Q02085 mus musculu  |
| 24     | 7     |       | 264    | 7  | YDCV_ECOLI | P77505 escherichia  |
| 25     | 7     |       | 273    | 7  | YD39_MYCTU | Q10648 mycobacteri  |
| 26     | 7     | 0.8   | 281    | Н  | YHIR_HAEIN | P31777 haemophilus  |
| 27     | 7     |       | 284    |    | BCHO_RHOCA | P26174 rhodobacter  |
| 28     | 7     |       | 284    | Н  | YD39_MYCLE | P50474 mycobacteri  |
| 29     | 7     |       | 287    | Н  | YKFA_ECOLI | P75678 escherichia  |
| 30     | 7     | 0.8   | 297    | Н  | YPGA_PORGI | Q51834 porphyromon  |
| 31     | 7     | •     | 303    | Н  | GDFF_RAT   |                     |
| 32     | 7     | 0.8   | 326    | -  | LEU3_ARCFU | 029627 archaeoglob  |
| 33     | 7     |       | 338    | Н  | G3P_SCHMA  |                     |

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SAHH_ARATH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- COFACTOR: PYRIDOXAL PHOSPHATE.
-i- PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-87250494; PubMed-3036823; Pablilips M.A., Coffino P., Wang C.C.; Pablilips M.A., Coffino P., Wang C.C.; C.C.; Cloning and sequencing of the contthine decarboxylase gene from Trypanosoma brucei. Implications for enzyme turnover and selective diffuoromethylornithine inhibition., J. Biol. Chem. 262:8721-8727(1987).
                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                           Length 838;
                                                                                                                                                                                                                                                                                                                      0; Indels
                        SEQUENCE FROM N.A.
Pohl T.M., Pohl F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                     96816 MW; 473A69D9C10167AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) ORNITHINE DECARBOXYLASE (EC 4.1.1.17) (ODC).
                                                                                                                                                                                                                                                                                          1.1%; Score 9; DB 1; 100.0%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000183; Orn_DAP_Arg_decarbxylse. Pfam; PF00278; Orn_DAP_Arg_dec; 2. PRINTS; PR01179; ODADCRBXLASE. PRINTS; PR01182; ORNDCRBXLASE.
                                                                SIMILARITY: SOME, TO S.POMBE SPACID4.10.
                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; J02771; AAA30218.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00878; ODR_DC_2_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF POLYAMINE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J02771; AAA30219.1; -.
                                                                                                                                                                                                EMBL; 228304; CAA82158.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Trypanosoma brucei brucei.
                                                                                                                                                                                                                                                                                                     Local Similarity 100.
nes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                         SGD; S0001787; YKR079C.
Hypothetical protein.
SEQUENCE 838 AA, 9681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A29309; DCUTOB.
InterPro; IPR000183;
                                                                                                                                                                                                                PIR; S38156; S38156
                                                                                                                                                                                                                                                                                                                                              682 LLIHEATLE 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DECARBOXYLASES
                                                                                                                                                                                                                                                                                                                                                               717 LLIHEATLE 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5702;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                         DCOR_TRYBB
P07805;
                                                                                                                                                                                                                                                                                           Query Match
Best Local §
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                                                                                                                                                                                                                                                                                                                      Matches
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STRAIN-CV. COLUMBIA;

MEDLINE-9812113; PubMed-9461215;

MEDLINE-98121113; PubMed-9461215;

Bevan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,

Bergkamp R., Dirkse W. van Staveren M., Stiekema W., Drost L.,

Ridley P., Hudson S.-A., Patel K., Murphy G., Piffanelli P.,

A. Wedler H., Wedler E., Wambutt R., Weitzeneger T., Pohl T.M.,

Lecharny A., Auborg S., Gy II., Kreis M., Lao N., Kavanagh T.,

Lecharny A., Auborg S., Gy II., Kreis M., Lao N., Kavanagh T.,

Hempel S., Kotter P., Entian K.-D., Rieger M., Schaeffer M., Funk B.,

Mueller-Auer S., Silvey M., James R., Montfort A., Pons A.,

Puigdomenech P., Douka A., Voukelatou E., Milloni D., Hatzopoulos P.,

Piravandi E., Obermaier B., Hilbert H., Duesterhoeft A., Moores T.,

A Jones J.D.G., Eneva T., Palme K., Benes V., Rechman S., Ansorge W.,

Cooke R., Berger C., Delseny M., Voet M., Volckaert G., Mewes H.-W.,

Riosterman S., Schueller C., Chalwatzis N.;

"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. COLUMBIA;
MEDLINE-20083488; PubMed=10617198;
MEDLINE-20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stlekema W., Entian K.-D., Terryn N.,
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgarther M., de Simone V., Obermaier B., Mache R., Mueller M.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
Langham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
PROSITE; PS00879; ODR_DC_2_2; 2.
Lyase; Decarboxylase; Pyridoxal phosphate; Polyamine biosynthesis.
BINDING 67 67 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
ACT_SITE 358 358 BY SIMILARITY.
ACT_SITE 358 40881 MW; 924A5AA6C4CD2C36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAHH_ARATH STANDARD; PRT; 485 AA.
023255; 081847;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S-ADENOSYL-L-HOMOCYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The isolation of an Arabidopsis thaliana cDNA clone encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. LANDSBERG ERECTA;
Belbahri L., Elleuch H., Villarroel R., Inze D., Thomas D.,
                                                                                                                                                                                                                                                                                                                            Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                            DB 1;
5. 7.3;
                                                                                                                                                                                                                                                                                                                            1.0%; Score 8; DB 1
100.0%; Pred. No. 7.3
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adenosyl-L-homocysteine hydrolase.";
(In) Plant Gene Register PGR99-139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROLASE) (ADOHCYASE).
SAHH OR AT4G13940 OR DL3010W.
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 391:485-488(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534 RVLGTLAA 541
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73 RVLGTLAA 80
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Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Morizen W., Morizen W., Morizen W., Morizen W., Caphausch M., Lamberth S., Van den Daele H., Breneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., Van Montagu W., Rogers J., Cronin A., Quail M., Bray-Allen S., Ray Montagu W., Rajandream M.-A., Lyne M., Benes V., Rechman S., Ray Mortey K., Mayes R., Bettett A., Rajandream M.-A., Lyne M., Benes V., Rechman S., Ray Mose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S., Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H., Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E., Ray Schenb M., Vandenbol M., Bargues M., Terol J., Torres A., Cheffor F., Cooke R., Berger C., Monfort A., Casacuberta E., Chokok R., Berger C., Monfort A., Casacuberta S., Cheffor F., Cooke R., Durnelle B., Bent E., Johnson S., Tacon D., Jesse T., Heimen D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Francs Perez A., Purnelle B., Bent E., Johnson S., Francs P., Bielke C., Ra Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Francs P. Beron M., Wilson R.K., de la Bastide M., Habermann K., Ratrealle P., Courtow W., Schott A., Schott K., Johnson D., Marray J., Sheet P., Cordes M., Abu-Threideh J., Schott K., Johnson D., Marker P., Bertley D., Fulton B., Miller N., Grock T., Kemp K., Minxe P., Bentley D., Fulton B., Miller N., Grock T., Kemp K., Marker J., Fulton L., Radards T., Layman D., Autonoju B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ray Marker J., Shody M., Hasegawa A., Hameed A., Lodhi M., Johnson A., Grant S., Shohdy N., Martjensen R., McCombie W. R., Chon M., Martjensen R., Marra M., Martjensen R., McCombie W. R., Shohdy N., Marselawa R., Hallana." R., Farent M., Martjensen R., McCombie W. R., Lodhi M., Julia R., Pallana." R., Farent M., Martjensen R., Marker H., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. LANDSBERG ERECTA;
2hang H., Forde B.G.;
"Identification of novel nitrate-inducible genes from Arabidopsis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-1997) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: ADENOSYLHOWCCYSTEINE IS A COMPETITIVE INHIBITOR OF S-ADENOSYLL-WETHININE-DEPENDER METHYL TRANSFRAME REACTIONS; THEREFORE ADENOSYLHOWCCYSTEINASE MAY PLAY A KEY ROLE IN THE CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR CONCENTRATION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)O -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i-- PATHWAY: ACTIVATED METHYL CYCLE.
-i-- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-i-- SIMILARITY: BELONGS TO THE ADENOSYLHOMOCYSTEINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAD (POTENTIAL).
E -> Q (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
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PROSITE; PS00738; ADOHCYASE_1; 1.
PROSITE; PS00739; ADOHCYASE_2; 1.
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EMBL; AL161537; CAB78436.1; -.
EMBL; Z97059; CAB09795.1; -.
InterPro; IPR000043; Ado_hcyase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 402:769-777(1999).
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                                                                                                                                     Gaps
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-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)O = ADENOSINE + L-HOMOCYSTEINE.
                                                                                                                                                                                                                                                                                                                                                                                                                        Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle). Bukaryota, Viitdiplantae; Streptophyta; Embryophyta; Trachophyta; Subtractophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-94218405; PubMed-8165255;
Schroeder G., Waitz A., Hotze M., Schroeder J.;
"CDNA for S-adenosyl-L-homocysteine hydrolase from Catharanthus
                                                                                                                                                                                                                                                                                                                   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S-ADENOSYL-L-HOMOCYSTEINE
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A -> R (IN REF. 4).
E -> Q (IN REF. 4).
T -> R (IN REF. 4).
; 1113270A0F46C86C CRC64;
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50CC0E99A9F66C51 CRC64;
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8.2;
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. 8.2;
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SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
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Pred. No.
                                                                                                   Score 8; I
Pred. No.
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NP_BIND 263 294 NAD (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Physiol. 104:1099-1100(1994).
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InterPro; IPR000043; Ado_hcyase.
InterPro; IPR000205; NAD_binding.
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                                                    53378 MW;
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100.0%;
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Best Local Similarity 100..
Best Similarity 100..
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NCBI_TaxID=4058;
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485 AA;
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Best Local Similarity
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P35007;
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HYDROLASE) (ADOHCYASE).
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                                                                                                                              NCBI_TaxID=4043;
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Michalowski C.B., Bohnert H.J.;

Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF
S-ADENOSYL-L-METHININE-DEPENDENT METHYL TRANSFERASE REACTIONS;
THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE
CONTROL OF METHILATIONS VIA REGULATION OF THE INTRACELLUBAR
CONCENTRALTION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)0 =
ADENOSINE + L-HOMOCYSTEINE.
                                                                                                                                                                                                                                                                                                                                                              Mesembryanthemum crystallinum (Common ice plant).
Westaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S-ADENOSYL-L-HOMOCYSTEINE
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01-OCT-1993 (Rel. 27, Last sequence update)
20-AGG-2001 (Rel. 40, Last annotation update)
ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S-ADENOSYL-L-HOMOCYSTEINE
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    Indels
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    Mismatches
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100.0%; Pred. No.
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NP_BIND 263 294 NAD (POTI
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    Conservative
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                                            DATLLIHE 686
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SAHH_MESCR
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                                                                                                                                                                                                                                                                                                                          Kawalleck P., Plesch G., Hahlbrock K., Somssich I.E.; "Induction by fungal elicitor of S-adenosyl-L-methionine synthetase and S-adenosyl-L-homocysteine hydrolase mRNAs in cultured cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Mol. Biol. 12:227-234(1989).
-!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS; THEREPORE ADENOSYLEOMOCYSTEIRASE MAY PLAY A KEY ROLE IN THE CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR
Petroselinum crispum (Parsley) (Petroselinum hortense).
Rukaryota: Viridiplantae: Streptophyta: Bubryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
Asteridae: euasterids II: Apiales: Apiaceae; Petroselinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 259-485 FROM N.A. Somssich I.E., Bollmann J., Hahlbrock K., Kombrink E., Schulz W.; Somssich I.E., Bollmann J., Hahlbrock K., Kombrink E., Schulz W.; Polfferential early activation of defense-related genes in elicitor-treated parsley cells."; Plant Mol. Biol. 12:227-234(1989).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S-ADENOSYL-L-HOMOCYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- TISSUE SPECIFICITY: MAINLY IN FLORAL BUDS AND STEMS.
-i- SIMILARITY: BELONGS TO THE ADENOSYLHOMOCYSTEINASE FAMILY.
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L -> C (IN REF. 1; AAA33855).
; 05E926516C2E08E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)O ADENOSINE + L-HOMOCYSTEINE.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 89:4713-4717(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAD (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0%; Score 8; DB 1; 0.0%; Pred. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         485 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 8.3
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONCENTRATION OF ADENOSYLHOMOCYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; NAD; One-carbon metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- PATHWAY: ACTIVATED METHYL CYCLE.
-!- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                             TISSUE=Leaf;
MEDLINE=92262510; PubMed=1374911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00738; ADOHCYASE_1; 1. PROSITE; PS00739; ADOHCYASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M81885; AAA33856.1; -.
EMBL; M62756; AAA33855.1; -.
InterPro; IPR000043; Ado_hcyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 leaves of Petroselinum crispum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53181 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SPECIES-N.sylvestris;
Mitsui S., Wakasugi T., Sugiura M.;
Mitsui S., Wakasugi T., Sugiura M.;
Mitsui S., Wakasugi T., Sugiura M.;
MacDNA encoding the 57 kDa subunit of a cytokinin-binding protein
complex from tobacco: the subunit has high homology to S-adenosyl-L-
complex from tobacco: the subunit has high homology to S-adenosyl-L-
complex from tobacco: the subunit has high homology to S-adenosyl-L-
complex from tobacco: the subunit of a cytokinin-binding protein
a.4.1089-1096(1993).
                                                                                                                                                                                                                                                   Plant Cell Physiol. 34:1089-1096(1993).

-!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF S-ADENOSYL-L-METHIONINE-DEFENDENT METHYL TRANSFERASE REACTIONS; THEREFORE ADENOSYL-L-MOCYSTEINE MAY PLAY A KEY ROLE IN THE CONTROL OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR CONCENTRATION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)O = ADENOSINE + L-HOMOCYSTEINE.

-!- COPACTOR: NAD (BY SIMILARITY).

-!- PATHWAY: ACTIVATED METHYL CYCLE.

-!- PATHWAY: ACTIVATED METHYL CYCLE.
SPECIES-N.tabacum; STRAIN-CV. BRIGHT YELLOW 4;
Tanaka H., Masuta C., Kataoka J., Kuwata S., Koiwai A., Noma M.;
Inducible expression by plant hormones of S-adenosyl-homocysteine
hydrolase gene from Nicotiana tabacum during early flower bud
formation in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1993 (Rel. 27, Created)
                                                                                                   Plant Sci. 113:167-174(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D45204; BAA08142.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROLASE) (ADOHCYASE).
SAHH OR SHH OR SH6.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
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P32112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
SEQUENCE
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         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                       Arch. Biochem. Biophys. 317:201-207(1995).

-!- FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF S-ADENOSYL-L-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS; THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE CONTENTRATION OF METHYLATIONS VIA REGULATION OF THE INTRACELLULAR CONCENTRATION OF ADENOSYLHOMOCYSTEINE (BY SIMILARITY).

-!- CONCENTRATION OF ADENOSYLHOMOCYSTEINE (H 2)O = ADENOSINE A L-HOMOCYSTEINE + H(2)O = ADENOSINE + L-HOMOCYSTEINE - + (2)O = ADENOSINE A CTIVATED METHYL CYCLE.

-!- COPACTOR: NAD (BY SIMILARITY).

-!- PATHWAY: ACTIVATED METHYL CYCLE.

-!- PATHWAY: ACTIVATED METHYL CYCLE.

-!- INDUCTION: BY INFECTION WITH B.CINBERA.
                                       Phalaenopsis sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;
Epidendroideae; higher Epidendroideae; Vandeae; Aeridinae;
                                                                                                                                                                                             MEDLINE-95177653; PubMed-7872785; Pretsig-function of the control of bibenary synthase and S-adenosylhomocysteine and expression of bibenary synthase and S-adenosylhomocysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana sylvestris (Mood tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Nicotiana.
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01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ADENOSYLHOWCXSTEINASE (EC 3.3.1.1) (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) (CYTOKININ BINDING PROTEIN CBP57).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 294 NAD (POTENTIAL).
485 AA; 53141 MW; 1EB2CA5AD63AF233 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.0%; Score 8; DB 1
100.0%; Pred. No. 8.2
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicotiana tabacum (Common tobacco), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase; NAD; One-carbon metabolism.
NP_BIND 263 294 NAD (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000043; Ado_hcyase.
Pfam; PF00670; AdoHcyase; 1.
PROSITE; PS00738; ADOHCYASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00739; ADOHCYASE_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X79905; CAA56278.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.0
Best Local Similarity 100.
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
     HYDROLASE) (ADOHCYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4097, 4096;
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phalaenopsis.
NCBI_TaxID=36900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           679 DATLLIHE 686
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                                                                                                                                                                                                                                                                             hydrolase.
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SEQUENCE
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
Triticeae, Triticum.
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0
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15-DEC-1998 (Rel. 37, Last annotation update)
ADENOSYLHOMOCYSTEINASE (EC 3.3.1.1) (S-ADENOSYL-L-HOMOCYSTEINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richards K.D., Gardner R.C.;
Submitted (XXX-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                263 294 NAD (POTENTIAL).
485 AA; 53104 MW; AA6D6844E9DF0A5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.0%; Score 8; DB 1
100.0%; Pred. No. 8.2
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Hydrolase, NAD, One-carbon metabolism.
NP_BIND 263 294 NAD (POTE
                                                                                                                                                                                                                          EMBL, D49804; BAA23164.1; -.
EMBL, D16138; BAA03709.1; -.
InterPro; IPR000043; Ado_hcyase.
Jem, PF00670; AdoHcyase; 1.
PROSITE; PS00738; ADOHCYASE_1; 1.
PROSITE; PS00739; ADOHCYASE_2; 1.
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between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                829 ADAPVALV 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
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ID MDR2_CRIGR
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                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-! SIMILARITY: CONTAINS 2 ANK REPEATS.
-! SIMILARITY: CONTAINS 1 PH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
FUNCTION: ADENOSYLHOMOCYSTEINE IS A COMPETITIVE INHIBITOR OF S-ADENOSYL-1-METHIONINE-DEPENDENT METHYL TRANSFERASE REACTIONS; THEREFORE ADENOSYLHOMOCYSTEINASE MAY PLAY A KEY ROLE IN THE CONTROL OF METHYLLATIONS VIA REGGLATION OF THE INTRACELLULAR CONCENTRATION OF ADENOSYLHOMOCYSTEINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96281124; Pubmed=8724849; Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.; Nagase T., Seki N., Ishikawa K.-I., Tanaka A., Nomura N.; Preddiction of the coding sequences of unidentified human genes. The coding sequences of 40 new genes (KIAA0161-KIAA0200) deduced analysis of cDNA clones from human cell line KG-1."; DNA Res. 3:17-24(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE ADENOSYLHOMOCYSTEINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-97336055; PubMed-9192850;
Elkahloun A.G., Krizman D.B., Wang Z., Hofmann T.A., Roe B.,
                                                                                                                           CATALYTIC ACTIVITY: S-ADENOSYL-L-HOMOCYSTEINE + H(2)O ADENOSINE + L-HOMOCYSTEINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 485;
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97FE208E3A6874ED CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 8; L
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase; NAD; One-carbon metabolism.
NP_BIND 263 294 NAD (POTE
                                                                                                                                                                                                       PATHWAY: ACTIVATED METHYL CYCLE. SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.0%; Sco.
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000043; Ado_hcyase.
Pfam; PF00670; AdoHcyase; 1.
PROSITE; PS00738; ADOHCYASE_1; 1.
PROSITE; PS00739; ADOHCYASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L11872; AAA34303.1;
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Best Local Similarity
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SEQUENCE
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the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endicott J.A., Sarangi F., Ling V.; "Complete cDNA sequences encoding the Chinese hamster P-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertębrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN REF. 2).
MISSING (IN REF. 2).
B8E42631BC06D5DC CRC64;
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01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN 2 (P-GLYCOPROTEIN 2).
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Mol. Cell. Biol. 7:4075-4081(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; Repeat; ANK repeat.
                                                                                                                                                                                                                                                                                                              PRINTS; PR00406; REVINTRACTNG.
PRINTS; PR00449; RASTRNSFRNG.
SMART; SM00248; ANK; 1.
SMART; SM00105; ArfGap; 1.
SMART; SM00105; ArfGap; 1.
SMART; SM0010; SMall_GTPASe; 1.
PROSITE; PS50088; ANK_REP_REGION; 1.
PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANK 1.
ANK 2.
                                                                                                                                                                                                InterPro; IPR001806; Ras_trnsfrmng.
InterPro; IPR003575; Small_GTPase.
InterPro; IPR001164; Znf_GCS.
Pfam; PF00023; ank; 2.
Pfam; PF01412; ArfGap; 1.
Pfam; PF00169; PH; 1.
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MEDLINE=92135896; Pubmed=1685679;
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                                                                                                                  EMBL; D79989; BAA11484.1; -. EMBL; U81031; AAC39522.1; -. InterPro; IPR002110; ANK. InterPro; IPR001849; PH.
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Best Local Similarity 100.
Matches 8; Conservative
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NCBI_TaxID=41882;
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SEQUENCE 12
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or send an email to license@isb-sib.ch).
FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROFEIN.
MISCELLANEOUS: PGP ISOFORMS DIFFER IN THEIR DRUG TRANSPORT
CAPABILLITES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 APPARENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                   SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00382; AAA; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 2.
ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 8.1 KDA PROTEIN IN NDHF-PSBD INTERGENIC REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta; Mesostigmatophyceae;
Mesostigmatales; Mesostigmataceae; Mesostigma.
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1276 AA; 141057 MW; 5096B1385628812D CRC64;
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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100.0%; Pred. No. 19;
ative 0; Mismatches
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InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001140; ABC_trnsportr_tmem.
InterPro; IPR001687; ATP_GTP_A.
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                                                                                                                                       (ABC TRANSPORTERS). MDR SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
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Best Local Similarity 100...
8; Conservative
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1075
635
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Q9MUR2;
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REPEAT
REPEAT
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ID YCX4_P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                 Lemieux C., Otis C., Turmel M.; "Ancestral chloroplast genome in Mesostigma viride reveals an early branch of green plant evolution."; Nature 403:649-652(2000).
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129 AA; 14301 MW; EDDEEF121B86F0D3 CRC64;
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; Chloroplast.
SEQUENCE 71 AA; 8147 MW; 9608379E175B0319 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRO8_HCMVA STANDARD; PRT; 129 AA. P16806; 01-AUG-1990 (Rel. 15, Created) 01-AUG-1990 (Rel. 15, Last sequence update) 01-FBB-1991 (Rel. 17, Last annotation update) HYPOTHETICAL PROTEIN IRL8 (TRL8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.8%; Score 7; DB 1;
100.0%; Pred. No. 16;
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.8%; Score 7; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                               STRAIN=NIES-296;
MEDLINE=20150907; Pubmed=10688199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Betaherpesvirinae; Cytomegalovirus.
NCBI_TaxID=10360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X17403; CAA35456.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAA35302.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF166114; AAF43891.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S09757; S09757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
SEQUENCE FROM N.A.
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**779 EERREKR 785** 

à a

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                             Ictalurid herpesvirus 1 (Channel catfish virus) (CCV). Viruses; dsDNA viruses, no RNA stage; Herpesviridae; unclassified Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M75136; AAA88145.1; -.
PIR; G36790; G36790.
Hypothetical protein.
SEQUENCE 129 AA: 14346 MW; DA7ECE85FECD4E9E CRC64;
                                                                                                                                                                                                                                                                                    Davison A.J.;
"Channel catfish virus: a new type of herpesvirus.";
Virology 186:9-14(1992).
                             VG42_HSVI1 STANDARD; PRT; 129 AA. 000101; 01-DEC-1992 (Rel. 24, Last sequence update) 01-DEC-1992 (Rel. 24, Last sequence update) 01-DEC-1992 (Rel. 24, Last annotation update) HYPOTHETICAL GENE 42 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.8%; Score 7; DB 1;
100.0%; Pred. No. 27;
Live 0; Mismatches
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-AUBURN 1;
MEDLINE-92087490; Pubmed-1727613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.8
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 QRRGVRD 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 QRRGVRD 38
RESULT 15
VG42_HSVI1
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Search completed: March 29, 2002, 10:24:41 Job time: 138 sec

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826
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1 MWALCSLLRSAAGRTMSQGR.......EPQQKRAHTEEPQAKKVRAQ
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                      219241 segs, 76174552 residues
                                                  OM protein - protein search, using sw model
                                                                                                                                                                                OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                             US-09-988-687-2
                                                                                                                                                                                                                                                0
                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                  Word size :
                                                                                                                                                         Sequence:
                                                                                                                                                                                                                        Searched:
                                                                           Run on:
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Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

219241

Total number of hits satisfying chosen parameters:

pirl:\* pir2:\* pir3:\* pir4:\* PIR\_68:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|               |        | æ              |                       |    |        |                    |
|---------------|--------|----------------|-----------------------|----|--------|--------------------|
| Result<br>No. | Score  | Query<br>Match | Ouery<br>Match Length | DB | ID     | Description        |
|               |        |                | 1                     | ;  | 1      |                    |
| Н             | 11     | 1.3            | 808                   | 7  | T38051 | hypothetical prote |
| 7             | 10     | ٠              | 837                   | 7  | F96561 | unknown protein [i |
| c             | O      | •              | 838                   | ~  | S38156 | hypothetical prote |
| 4             | 8      | 1.0            | 147                   | ~  | D75073 | ¥                  |
| J.            | 80     | 1.0            | 216                   | ~  | 25     | •—                 |
| 9             | 80     |                | 255                   | ~  | T35217 |                    |
| 7             | 8      | 1.0            | . 260                 | 7  | 511    | _                  |
| 8             | 8      | 1.0            | 280                   | Н  | A71022 |                    |
| 6             | 8      | 1.0            | 307                   | ~  | A71057 | 41                 |
| 10            | 80     | 1.0            | 440                   | 7  | C85785 | probable thiosulfa |
| 11            | 80     | 1.0            | 445                   | Н  | DCUTOB | ornithine decarbox |
| 12            | 80     | 1.0            | 485                   | 7  | C71400 | adenosylhomocystei |
| 13            | 8      | 1.0            | 485                   | 7  | S71621 | adenosylhomocystei |
| 14            | 8      | 1.0            | 485                   | 7  | 838379 | adenosylhomocystei |
| 15            | 80     | 1.0            | 485                   | 7  | T06764 | adenosylhomocystei |
| 16            | 80     | 1.0            | 643                   | 7  | F84117 | hypothetical prote |
| 17            | œ<br>œ | 1.0            | 806                   |    | T35640 | ഗ                  |
| 18            | 8      | 1.0            | 686                   |    | C83035 | hypothetical prote |
| 19            | œ      |                | 1630                  | 7  | T00390 | KIAA0614 protein - |
| 20            | 7      |                | 106                   |    | T36932 |                    |
| 21            | 7      |                | 122                   |    | S40351 | Ig kappa chain V-J |
| 22            | 7      |                | 129                   |    | S09757 | hypothetical prote |
| 23            | 7      | 0.8            | 129                   |    | 636790 | hypothetical prote |
| 24            | 7      | ٠              | 139                   |    | C83526 | _                  |
| 25            | 7      |                | 144                   | 7  | 98     | _                  |
| 56            | 7      |                | 144                   | ~  | œ      | _                  |
| 27            | 7      | 0.8            | 144                   | 7  | 283    | Ω.                 |
| 28            | 7      | ٠.             | 148                   | 7  | 25     | hypothetical prote |
| 53            | 7      | 0.8            | 149                   | 7  | C69393 | □                  |

| hypothetical | qlutathione peroxi | probable transmemb | merozoite surface | hypothetical prote | merozoite surface | merozoite surface | conserved hypothet | late expression fa | InaA protein - Esc | hypothetical prote | hypothetical prote | KorA protein - Str | hypothetical prote | hypothetical prote | hypothetical prote |
|--------------|--------------------|--------------------|-------------------|--------------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| T12803       | T44271             | T35112             | A45562            | T48828             | B49247            | C49247            | E82388             | T10392             | C64994             | B85863             | T01599             | H31844             | D84304             | A83310             | T36131 '           |
| ٥            |                    | . 7                | ~                 | 7                  | <b>ري</b>         | 7                 | 7                  | ∾.                 | ~                  | ~                  | 7                  | 7                  | . 5                | 7                  | 7                  |
| 156          | 167                | 167                | 171               | 189                | 197               | 197               | 209                | 211                | 216                | 216                | 239                | 241                | 247                | 250                | 250                |
| c            | . 0                | 0.8                | 0.8               | 0.8                | 0.8               | 0.8               | 0.8                | 0.8                | 0.8                | 0.8                | 0.8                | 0.8                | 0.8                | 0.8                | 0.8                |
| 7            |                    | 7                  | 7                 | 7                  | 7                 | 7                 | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  |
| 30           | 31                 | 32                 | 33                | 34                 | 35                | 36                | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

## ALIGNMENTS

| RESULT 1<br>T38051                                                                                                  |
|---------------------------------------------------------------------------------------------------------------------|
| hypothetical protein SPACID4.10 - fission yeast (Schizosaccharomyces pombe)                                         |
| c;species: sciizosaccharomyces pombe<br>C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 |
| C; Accession: T38051                                                                                                |
| R;Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.                                             |
| submitted to the EMBL Data Library, February 1995                                                                   |
| A. Reference number: 221765                                                                                         |
| A) ACCESSION: 138051                                                                                                |
| A;Status: preliminary; translated from GB/EMBL/DDBJ<br>A:Molecule type: DNA                                         |
| A; Residues: 1-809 < LYE>                                                                                           |
| A; Cross-references: EMBL: Z69239; PIDN: CAA93219.1; GSPDB: GN00066; SPDB: SPAC1D4.10                               |
| A; Experimental source: strain 972h-; cosmid c1D4                                                                   |
| C;Genetics:                                                                                                         |
| A; Gene: SPDB:SPAC1D4.10                                                                                            |
| A; Map position: 1                                                                                                  |
| A;Introns: 129/1                                                                                                    |
|                                                                                                                     |
| Query Match 1.3%; Score 11; DB 2; Length 809;                                                                       |
| 0%; Pred. No. 0.016;                                                                                                |
| Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                         |
| Qy 681 TLLIHEATLED 691                                                                                              |
|                                                                                                                     |
| Db 704 TLIHEATLED 714                                                                                               |
|                                                                                                                     |
|                                                                                                                     |

RESULT F96561

unknown protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001
C;Accession: F96561
R;Theologis. A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakon, H.; Shin, P.; Southwick, A.M.; Sun, H.; Tallc A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallc A;Atcession: F96561
A;Accession: F96561
A;Accession: F96561
A;Accession: F96561
A;Accession: F96561
A;Reidues: preliminary
A;Molecule type: DNA
A;Reidues: 1-837 <STO>
A;Cross-references: GB:AE005173; NID:96850339; PIDN:AAF29402.1; GSPDB:GN00141

```
C; Species: Pyrococcus abyssi
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C; Accession: G75111
R; anonymous, Genoscope
S; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A; Reference number: A75001
A; Reference number: A75001
A; Reference number: Data
A; Retus: preliminary
A; Molecule type: DNA
A; Residues: 1-260 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SC5C7.10c SC5C7.10c - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Sccession: T35217
R; Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1998
A; Reference number: Z21572
A; Reference number: Z21572
A; Reference number: Z21572
A; Reference number: Z21572
A; Residues: L255 SEE>
A; Residues: L-255 SEE>
A; Cross-references: EMBL; AL031515; PIDN: CAA20622.1; GSPDB: GN00070; SCOEDB: SC5C7.10c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                A; Accession: T23258
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-216 <WIL>
A; Cross-references: EMBL:Z77133; PIDN:CAB00867.1; GSPDB:GN00028; CESP:K03A11.3
A; Experimental source: clone K03A11
C; Genetics:
                                                  hypothetical protein K03A11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein PAB1906 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: strain A3(2)
C; Genetics:
A; Gene: SC5C7.10c
C; Superfamily: conserved hypothetical protein MJ1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 8; DB 2;
Pred. No. 7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.0%; Score 8; DB 2
Best Local Similarity 100.0%; Pred. No. 8.1
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                       submitted to the EMBL Data Library, July 1996 A; Reference number: 219717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.0%; Score 8;
100.0%; Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.0°
Best Local Similarity 100°
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: X
A; Introns: 136/3; 168/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                544 VSHLHADH 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP: K03A11.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 SEFNRYLF 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: T23258
R; Swinburne, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rianonymous, Genoscope
submitted to the EMBL Data Library, July 1999
Submitted to the EMBL Data Library, July 1999
A. Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A. Reference number: A75001
A. Accession: D75073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Rasidues: 1-147 <KAW>
A;Cross-references: GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB49889.1; PID:g545846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Cross-references: EMBL:228304; NID:9486556; PID:9486557; GSPDB:GN00011; MIPS:YKR079c A)Experimental source: strain S288C C;Genetics: C;Genetics: A,Gene: MIPS:YKR079c. A,Gene: MIPS:YKR079c. A,Map position: 11R
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                                                                                                                                                                                                                                                                                                                                                          hypothetical protein YKR079c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 0.3 May-1994 #sequence_revision 0.3 May-1994 #text_change 29-oct-1999
C;Accession: S38156
R;Pohl, T.M.; Pohl, F.M.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S37897
A;Accession: S38156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A,Gene: PAB0657
C.Superfamily: protein kinase C inhibitor; histidine triad homology
F;3-99/Domain: histidine triad homology <HIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                         Length 837
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                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 838;
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                                                                                                                      DB 2;
0.19;
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o. 5;
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                                                                                                                      Score 10; DB; Pred. No. 0.10; Mismatches
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1.1%; Score 9; DB 2
Best Local Similarity 100.0%; Pred. No. 2.1
Matches 9; Conservative 0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches
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                                                                                                                    1.2%; ;
100.0%;
                                                                                                                      Query Match 1.2
Best Local Similarity 100.
Matches 10; Conservative
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515 SLLLDCGEGT 524
                                                                                                                                                                                                                       511 SLLLDCGEGT 520
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A; Residues: 1-838 <POH>
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C;Genetics:
A;Gene: F915.1
A;Map position:
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D.J.; May
K.; Apoda
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A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z2789
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C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999
C;Accession: A29309
R;Phillips, M.A.; Coffino, P.; Wang, C.C.
A;Fille: Cloning and sequencing of the crnithine decarboxylase gene from Trypanosoma A;Reference number: A29309; MuID:87250494
                                                                                                                                                                                                                               C:Species: Escherichia coli
C:Species: Escherichia coli
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
C:Accession: 085785
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, I. 11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, R. Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adenosylhomocysteinase (EC 3.3.1.1) [similarity] - Arabidopsis thaliana NyAlternate names: protein DL3010W; S-adenosyl-L-homocysteine hydrolase C;Species: Arabidopsis thaliana (mouse-ear cress) A;Variety: columbia C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-445 CPB:10-2771; NID:9162173; PIDN:AAA30218.1; PID:9162174
A; Cross-references: GB:10-2771; NID:9162173; PIDN:AAA30218.1; PID:9162174
C; Superfamily: ornithine decarboxylase
C; Keywords: carbon-carbon lyase; araboxy-lyase; phosphoprotein; polyamine l'
F; 89 Phinding site: pyridoxal phosphate (Lys) (covalent) #status predicted
F; 380/Active site: Cys (shared with dimeric partner) #status predicted
  Gaps
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  Indels
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100.0%; Pred. No. 13;
iive 0; Mismatches
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  Mismatches
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Best Local Similarity 100.
Matches 8; Conservative
  8; Conservative
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A; Residues: 1-440 <STO>
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                                                                                    1111111
202 KVVYSGDT
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                                                       660 KVVYSGDT
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A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49608.1; PID:g545811
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable sulfatase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: A71057
K;Rwarabayasii, Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y.; Hino, Y.; Yamamoto, S.; Sekin
Yamazaki, J.; Kushida, N.; Oguchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: strain 073
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Date: 10-Sep-1999
R;Advarabayasi, Y; Sawada, M; Horikawa, H; Haikawa, Y; Hino, Y; Yamamoto, S; Seki M; Ohfuku, Y; Funahashi, T; Tanaka, T; Kudoh, Y; Yamazaki, J; Kushida, N; Oguch A; Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137
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                                                 C;Genetics:
A;Gene: PAB1906
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: PH1470
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-280 <KAW>A;Residues: 1-280 <KAW>A;Cross-references: GB:AP000006; NID:93236133; PIDN:BAA30577.1; PID:93257894
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A; Experimental source: strain OT3
                                                                                                                                                                                                                                                      Gaps
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C;Superfamily: conserved hypothetical protein MJ1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PH1470 - Pyrococcus horikoshii
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                                                                                                                                                                                            1.0%; Score 8; I
100.0%; Pred. No.
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Matches 8; Conservative 0
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Best Local Similarity
Matches 8; Conserv
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C; Species: Triticum aestivum (common wheat)
C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C; Accession: T06764
R;Richards, K.D.; Gardner, R.C.
submitted to the EMBL Data Library, March 1993
A; Description: The influence of aluminium on histone, heat shock and S-adenosyl-L-hom A; Reference number: 215795
                                                                                                                                                                                                                                                                                                                                                                                                               Rischroeder, G.; Waitz, A.; Hotze, M.; Schroeder, J.
submitted to the EMBL Data Library, October 1993
A; Description: CDNA for stress-induced S-adenosyl-L-homocysteine hydrolase from Madag
A; Reference number: S38379
                                                                                                                                                                                                                                                  N;Alternate names: S-adenosyl-L-homocysteine hydrolase
C;Species: Catharanthus roseus (Madagascar periwinkle)
C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-485 <SCH>
A;Cross-references: EMBL:226881; NID:g407411; PIDN:CAA81527.1; PID:g407412
C;Genetics:
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Status: 1-485 <RIC>
A.Cross-references: EMBL:L11872; NID:g170772; PIDN:AAA34303.1; PID:g170773
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: adenosylhomocysteinase
C;Keywords: NAD; thloether hydrolase
F;263-292/Region: beta-alpha-beta NAD nucleotide-binding fold
F;86,120/Active site: Cys #status predicted
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C;Superfamily: adenosylhomocysteinase
C;Keywords: NAD; thioether hydrolase
F;263-292/Region: beta-alpha-beta NAD nucleotide-binding fold
F;86,120/Active site: Cys #status predicted
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    Madagascar periwinkle

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Job time: 138 sec
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Best Local Similarity 100...
8; Conservative
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N;Alternate names: S-adenosyl-L-homocysteine hydrolase
C;Species: Phalaenopsis sp.
C;Dete: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 22-Jun-1999
C;Accession: S71621
Arcession: S71621
Arch: Biochem: Biophys: 317, 201-207, 1995
A;Title: The inducible 9,10-dihydrophenanthrene pathway: characterization and expression and express
                                                                                                              avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Mature 391, 485-488, 1998
A; Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans A; Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal A; Reference number: A71400; MUID:99121113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA

A; Residues: 1-885 < CEV.7

A; Cross-references: GB: Z97335; NID: 92244747; PIDN: CAB10173.1; PID: 92244750

B; Belbahri, L.; Elleuch, H.; Villaroel, R.; Inze, D.; Thomas, D.; Thomasset, B.

Bjant Physiol. 121, 313, 1999

A; Title: The Isolation of an Arabidopsis thaliana cDNA clone encoding S-adenosyl-L-homocy. A; Reference number: Z25409
                                      R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dir
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Gie
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.
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A;Status: nucleic acid sequence not shown
A;Racluca: 1-485 CPRE>
A;Expessitues: 1-485 CPRE>
A;Cross-references: EMBL:X79905; NID:g758246; PIDN:CAA56278.1; PID:g758247
A;Experimental source: clone SHH511
C;Superfamily: adenosylhomocysteinasse
C;Superfamily: denosylhomocysteinasse
C;Steyords: NAD; thioether hydrolass
F;263-292/Region: beta-alpha-beta NAD nucleotide-binding fold
F;86,120/Active site: Cys #status predicted
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F;263-292/Region: beta-alpha-beta NAD nucleotide-binding fold
F;86,120/Active site: Cys #status predicted
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A;Molecule type: mRNA
A;Residues: 1-485 EMBL.AF059581; PIDN:AAC14714.1
A;Cross-references: EMBL:AF059581; PIDN:AAC14714.1
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100.0%; Pred. No. 14;
tive 0; Mismatches
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100.0%; Pred. No. 14;
tive 0; Mismatches
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Matches 8; Conservative
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C; Accession: C71400; T51608
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Copyright (c) 1993 - 2000 Compugen Ltd.
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| Human ORFX ORF2401<br>Human phosphatase | Arabidopsis thalia | is thal  | S      | pro      | S        | is       |          | Arabidopsis S-aden | О        | Arabidopsis thalia | Arabidopsis thalia | 5        | įs       | Ø        | Arabidopsis thalia | ຜ        | Zea mays protein f | Arabidopsis thalia | Arabidopsis thalia | S        | a        | #372     | Peptide #3830 enco | 9  | Peptide #5977 enco | Peptide #6620 enco | Pinus radiata tran | te       | Human gene 2 encod | Human colon cancer | secrete | Human gene 2 encod |
|-----------------------------------------|--------------------|----------|--------|----------|----------|----------|----------|--------------------|----------|--------------------|--------------------|----------|----------|----------|--------------------|----------|--------------------|--------------------|--------------------|----------|----------|----------|--------------------|----|--------------------|--------------------|--------------------|----------|--------------------|--------------------|---------|--------------------|
| AAB42637<br>AAB85355                    | AAG08256           | AAG08255 | $\sim$ | AAG34061 | AAG22957 | AAG40087 | AAG41408 | AAW01459           | AAG34060 | AAG40086           | AAG41407           | AAR26500 | AAG22956 | AAG41406 | AAG40085           | AAG08254 | AAG34059           | AAG49847           | AAG49846           | AAG49845 | AAM39023 | AAM17295 | AAM29793           |    | AAM19543           | AAM32583           |                    | AAY87065 |                    | 4                  | П       | AAE06134           |
| 21                                      | 21                 | 21       | 21     | 21       | 21       | 21       | 21       | 17                 | 21       | 21                 | 21                 | 13       | 21       | 21       | 21                 | 21       | 21                 | 21                 | 21                 | 21       | 22       | 22       | 22                 | 21 | 22                 | 22                 | 21                 | 21       | 22                 | 21                 | 21      | 22                 |
| 377                                     | 394                | 422      | 449    | 450      | 467      | 467      | 467      | 485                | 485      | 485                | 485                | 486      | 489      | 497      | 208                | 509      | 510                | 790                | 848                | 922      | 1632     | 20       | 20                 | 25 | 57                 | 57                 | 81                 | 98       | 98                 | 66                 | 108     | 108                |
| 1.0                                     | 1.0                |          | •      |          | •        |          | •        | 1.0                | •        | 1.0                |                    |          |          |          |                    | 1.0      |                    |                    |                    |          |          |          |                    |    |                    | -                  |                    |          |                    |                    | 0.8     |                    |
| ထထ                                      | 80                 | 80       | æ      | œ        | œ        | œ        | æ        | æ                  | œ        | œ                  | æ                  | 80       | æ        | œ        | æ                  | œ        | 8                  | æ                  | œ                  | œ        | 80       | 7        | 7                  | 7  | 7                  | 7                  | 7                  | 7        | 7                  | 7                  | 7       | 7                  |
| 12                                      | 14                 | 15       | 16     | 17       | 18       | 19       | 20       | 21                 | 22       | 23                 | 24                 | 25       | 26       | 27       | 28                 | 29       | 30                 | 31                 | 32                 | 33       | 34       | 35       | 36                 | 37 | 38                 | 39                 | 40                 | 41       | 42                 | 43                 | 44      | 45                 |
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## ALIGNMENTS

Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer Human, prostate cancer predisposing gene; HPC2; chromosome 17p; gene therapy; peptide therapy; drug design. Rommens JM; Human prostate cancer predisposing protein HPC2 Pavtigian SV, Teng DHF, Simard J, AA. AAB07228 standard; protein; 826 99WO-US26055. (MYRI-) MYRIAD GENETICS INC. 98US-0107468. (first entry) WPI; 2000-376481/32. N-PSDB; AAA58453.

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AAY99850 RESULT

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cancer predisposing gene HPC2, which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This protein and its gene can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs.
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Local Similarity 100.0%; Pred. No. 0;
Hes 826; Conservative 0; Mismatches
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                                PEIIFLGTGSAIPMKIRNVSATLVNISPDTSLLLDCGEGTFGQLCRHYGDQVDRVLGTLA
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AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimilant; cardiant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidianemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy crotice acids can be used to express ORFX proteins in gene therapy proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic annemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinifiammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
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                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 3181-3182; 5507pp; English
990S-0127636.
990S-0127728.
20000S-0540763.
                                                                                                                                                                                               Leach M;
                                                                                                                                  (CURA-) CURAGEN CORP
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptrises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide which comprises one of the 5602 nuclectide comprises at least 15 nuclectides; or (b) a combination oligonuclectide comprises at least 15 nuclectides; or (b) a combination of an oligonuclectide comprises a least 15 nuclectides; or (b) a combination of sequence and an oligonuclectide comprises a 3'-end sequence complementary to the compliance of the comprises a 3'-end sequence complementary to a polynuclectide which comprises a 3'-end sequence defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the formation of the 5'-end sequence of the primers are also useful for the particularly full-length cDNAs. The primers are also useful for the particularly full-length cDNAs. The primers are also useful for the contact of the full-length but any specialised methods. AAH13613 to AAH136
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Yamamoto
T;
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Otsuki
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A,   Nagai K,
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T, Wakamatsu
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27-MG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
09-JUN-2000; 2000JP-0241899.
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Ishii S
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                                          OVVAAGSRDSGAALYVFSEFNRYLFNCGEGVQRLMQEHKLKVARLDNIFLTRMHWSNVGG
                                                                                                   LSGMILTLKETGLPKCVLSGPPQLEKYLEAIKIFSGPLKGIELAVRPHSAPEYEDETMTV
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Length 854;
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99.6%;
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19-APR-1999;
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15-JUL-1999;
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                                                                                                                                                                                                                   The present sequence is the protein produced from the murine prostate cancer predisposing gene HPC2, the human homologue of which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This protein and its gene can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs.
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                    Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
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100.0%; Pred. No. 3e-07;
ive 0; Mismatches 0; Indels
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                                                                                                                     Rommens JM;
                                                                                                                                                                                                 Disclosure; Page 151-152; 157pp; English.
                                                                                                                     Teng DHF, Simard J,
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990S-0123548.
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                                                                                                 GENETICS INC
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Best Local Similarity 100.
Matches 15; Conservative
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N-PSDB; AAA60390.
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                                                                                               (MYRI-) MYRIAD
                                                                                                                    Tavtigian SV,
Mus musculus.
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990S-0128714.
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990S-0130047.
      9905-0159330.
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9905-0160815.
9905-0160819.
9905-0160819.
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990S-0161406.
990S-0161359.
990S-0161360.
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99US-0161992
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Immunostimulant; antiinflammatory; cardiant; vulnerary; antiulcer; notropic; antiinflammatory; cardiant; vulnerary; antiulcer; antibartaint; antiparastic; chromobylvic; antiboqualmt; polynucleotides can be used in gene therapy and as vaccines, proteins and angiogenesis- modulators. The human secreted proteins and polynucleotides can be used for diagnosing (the susceptibility to) a pathological condition by determining the presence or amutation in the polynucleotide or determining the presence presence or a mutation in the polynucleotide or determining the presence presence or amount of expression of the protein. The polynucleotides and proteins can also be used in the treatment and diagnosis of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; immunosuppressive; immunostimulant; nootropic; antinoframatory; cardiant; vulnerary; antiulocry; antinoovulasant; antiparkinsonian; neuroprotective; antivoral; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; antiparasy; vaccine; chemotaxis-modulator; antiarteriosclerotic; cancer; immune system disorder; hyperproliferative disorder; infection; cardiovascular disorder; neurological disease; wound healing;
can be used in the treatment of cancer, psoriasis and restenosis. This ibecause they can be used to identify plant, insect and human homologues of the yeast genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The polynucleotide sequences given in AAA87666 to AAA87708 encodes the human secreted proteins given in AAB2565 to AAB25755. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide encoding a secreted protein useful for preventing, treating or ameliorating a medical condition -
                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein sequence encoded by gene 15 SEQ ID NO:68.
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Pred. No. 4.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides methods of identifying antifungal agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yeast; germination; proliferation; essential gene; antifungal agent; insecticide; herbicide; anti-proliferation drug; cancer; psoriasis; restenosis; YKR081C; YFR003C; YGR277C; YGR278W; YKR071C; YKR079C; YKR083C.
                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                      DB 21; Length 154;
0.089;
hes 0; Indels
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Pred. No. 0.08
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100.0%; Pre
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                                                       990S-0160815.
990S-0160980.
990S-0160981.
990S-0161404.
990S-0161405.
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99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
              99US-0160768.
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99US-0389341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB49964;
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                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                  511
                                                                                                                                                                                                                                                                                                                    Matches
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Moore PA;

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                cardiovascular disorders and neurological disease. They can also be used to promote wound healing and to fight infection. AAA87657 to AAA87665 and AAB25664 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antidiametic; antibacterial; cardiant; dermitological; neuroprotective; thrombolytic; coaquiant; nootropic; vasotropic; antipportatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                  ;
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  diseases of the immune system, hyperproliferative disorders,
                                                                                                                                                                         DB 21; Length 141; 9.7;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cancer associated protein sequence SEQ ID NO:1055.
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                                                                                                                                                                       1.0%; Score 8; DB 2
100.0%; Pred. No. 9.7
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            AAB43610 standard; Protein; 243 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-587533/55.
                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                 141 AA;
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                                                                                                                                                                                                                                                    67 SRDSGAAL 74
                                                                                                                                                                                                                                                                                         46 srdsgaal 53
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                                                                            invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB43610;
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                       RESULT 10
                                                                                                                                                                                                                Matches
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or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate haemostatic or thrombolytic activity, modulate haftenmation, cancers, cardiovascular disorders, neurological disease and antegonists and antegonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal cancers and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 4277~\mathrm{human} colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; colon cancer antigen; diagnosis; detection;
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                                                                                                                                                                                                                                                             DB 21; Length 243;
                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human colon cancer antigen protein SEQ ID NO:6391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA;
                                                                                                                                                                                                                                                           1.0%; Score 8; DB 2
100.0%; Pred. No. 16;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 7872-7873; 9803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG75627 standard; Protein; 245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barash SC, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                      8; Conservative
                                                                                                                                                               the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colorectal carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-235357/24.
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             298 TPPDPGAA 305
                                                                                                                                                                                                                                                                                                                                                                                  17 tppdpgaa 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG75627;
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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WO200153469-A2.
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25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB85355;
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           wulnerary; antipsoriatic; antiparkinsonian; organical inspectoriopic; vulnerary; antipsoriatic; antiarthritic; immunosuppressant; cardiant; immunosuppressant; cardiant; immunosuppressant; cardiant; immunosuppressive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidifiammatory; antidiaral; antidiametory; antidiametory; antidiametory; antidiametory; cancer; proliferative disorder; hypothyroid; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaris autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 open reading frame; ORFX; detection; cytostatic; hepatotropic;
            N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                ;
0
                                                                                                                               Length 245;
                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Human ORFX ORF2401 polypeptide sequence SEQ ID NO:4802.
                                                                                                                              DB 22;
                                                                                                                              Score 8; DB 2;
Pred. No. 16;
0; Mismatches
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                                                                                                                                                                                                                                                                                                              AAB42637 standard; Protein; 377 AA.
                                                                                                                   1.0%; Sur-
100.0%; Pre
0; /
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02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000WO-US08621
                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombosis; contraceptive
                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA, Leach M;
                                                                                                           Query Match
Best Local Similarity
8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-602362/57.
present invention.
                                                                             245 AA;
                                                                                                                                                                                             298 TPPDPGAA 305
                                                                                                                                                                                                                           tppdpgaa 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC76846
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                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2001
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                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                               AAB42637;
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                                                                                                                                                                                                                                                                                              AAB42637
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immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides human phosphatases (PP) and polynucleotides encoding the phosphatases. The polypeptides can be expressed by standard recombinant methodology. The PP are useful for treating a disease or
                                                                                                                                                                                                      nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholosterol ester storage, systemic lupus bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel phosphatases useful for treating diseases associated with decreased expression of functional phosphatases, e.g., Alzheimer's disease, Huntington's disease, immune disorders, and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phosphatase; PP; Alzheimer's disease; Huntington's disease; human; immune disorder; cancer; nootropic; immunomodulatory; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baughn MR, Hillman JL;
Mathur P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.0%; Score 8; DB 2
100.0%; Pred. No. 24;
tive 0; Mismatches
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Gandhi AR, Policky JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 91-92; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB85355 standard; Protein; 385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective; anticonvulsant.
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2000US-0184959.
2000US-0190142.
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Best Local Similarity 100.
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-451905/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 srdsqaal 290
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990S-0136392
990S-0136782
990S-0137528
990S-0137524
990S-0137724
990S-0138640
990S-0138840
990S-0139453
990S-0139453
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99US-0140823.
99US-0140991.
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99US-0142154.
99US-0142055.
99US-0142390.
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99US-0144086.
99US-0144325.
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990S-0144332.
990S-0144333.
990S-0144334.
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   25-MAY 1999;
28-MAY 1999;
28-MAY 1999;
01-70N 1999;
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16-70N 1999;
16-70N 1999;
16-70N 1999;
18-70N 1999;
19-70N 1999;
20-70N 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
condition associated with decreased expression of functional phosphatases. Compositions containing agonists or antagonists of PP may be used to treat a disease associated with decreased expression or overexpression of PP, respectively. Such diseases may include Alzheimer's disease, Huntington's disease, immune disorders, and cancers. The present sequence represents a human phosphatase.
                                                                                                                                                                                       Gaps
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                                                                                                                                                    Score 8; DB 22; Length 385;
Pred. No. 24;
0; Mismatches 0; Indels
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ID AAGG08256

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AGG08256;

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AGG08256;

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AGG08256;

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AGG08256;

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T7-OCT-2000 (first entry)

XX

YEAL 17-OCT-2000 (first entry)

XX

Protein identification; signal transdivation assay; genetic mapping; the remination assay; genetic mapping; XX

XX

YX

Protein identification; signal transdivation assay; genetic mapping; XX

XX

XX

BP1033405-A2.

XX

XX

D6-SEP-2000; 2000EP-0301439.

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XX

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PR

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PR

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PR

Z5-MAR-1999; 99US-0126746.

PR

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100.0%; Pre
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Best Local Similarity 100.
Matches 8; Conservative
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PR 21-ARC-19
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29-OCT-1999;
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PR 09-AuG-1999; 99US-0147433.
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Gaps

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Qy Db

Search completed: March 29, 2002, 10:22:53 Job time: 140 sec

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601892128

602426274

us-09-988-687-1.oli.rst

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E l'hases i to 676)

S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCMI76 row: d column: 01

High quality sequence stop: 672.

Location/Qualifiers

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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April 1, 2002, 09:30:21; Search time 1186.93 Seconds (without alignments) 22461.541 Million cell updates/sec
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BG822529 6027269966
BE383335 601298249
BE382335 601298249
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BF744169 7099f04 x
BG396395 602459323
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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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ö NT2 neuronal (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki Euteleostomi; Research Institute, cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute. Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J. Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and 480 61 accatatcgcaggcacccgccgccgcgaggccgcgcaaggacccgctgcggcacctg 120 321 ttaagtggaatgattcttactttaaaggaaaccgggcttccaaagtgtgtactttctgga 420 atagaactggctgtgcggccccactctgccccagaatacgaggatgaaaccatgacagtt 540 aaccggtatctcttcaactgtggagaaggcgttcagagactcatgcaggagcacaagtta 300 Gaps 81 1 atgtgggcgctttgctcgctgctgcggtccgcgggccggacgcaccatgtcgcagggacgc ACCATATCGCAGGCACCCGCCGCGCGCGCGCGCGCAAGGACCCGCTGCGGCACCTG cgcacgcgagagagagcgcggaccgtcgggggtgctccggcggcccaaacaccgtgtacctg CGCACGCGAGAGAGAGCGCGGACCGTCGGGGTGCTCCGGCGGCGCCCAAACACCGTGTACCTG AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA cotocacaactggaaaaatacotcgaagcaatcaaaatattttotggtocattgaaagga ö from uninduced Craniata; Vertebrata; E Catarrhini; Hominidae; Length 712; Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Y., Sugano, S., Isogai, T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarau, Chiba 292-0812, Japan
Tel: 81-438-52-3952
Fax: 81-448-52-3952
Fmail: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass se Score 639; DB 10; I Pred. No. 7.1e-297; /organism="Homo sapiens"
/db\_xref="taxon:9606"
/clone="NT2RM4002610"
/clone\_lib="NT2RN4"
/cell\_type="teratocarcinoma"
/cell\_tine="NT2"
/note="Vector: pME18SFL3; mRNA fr 25.8%; Scor. 100.0%; Pred. No. ... ... 0; Mismatches ų 134 Chordata; Primates; Location/Qualifiers 6 204 Isogai,T. HRI human cDNA project Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 712) Ö Conservative 198 Similarity 173 481 δ

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 666)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 81-438-52-3952
Email: genomics@hri.co.jp
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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ilarity 100.0%; Pred. No. 2e-282;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="THYRO1000421"
/clone=lb="THYRO1"
/tissue_type="thyroid glar
/note="Vector: pME185F13"
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Isogai, T.
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Contact: Takao Isogai
Genomics Laboratory
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 762)
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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/clone_lib="NT2RM4"
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Fax: 81-438-52-3952
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 791)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Score 601; DB 10;
Pred. No. 1.5e-278;
0; Mismatches 1;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/clone=lib="NIH_MGC_15"
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/note="0rgan: colon: Vector: p0TB7; Site_1: Xho1; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xho1 sites using the following 5/ adaptor: GGCACGAG(G). Size-selected 550bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
82 a 224 c 216 g 169 t
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Cound through the I.M.A.G.E. Consortium/LLNL
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Pred. No. 4.5e-278;
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             http://image.llnl.gov
Plate: LLCM1730 row: i column:
High quality sequence stop: 789.
Location/Qualifiers
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99.7%;
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Matches 770; Conserv
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/tissue_type="adrenal cortex carcinoma, cell line"
/lab_host="bH10B (phage-resistant).
/note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
NotI; Site_2: SalI; Cloned unidirectionally; oligo-dr
primed. Average insert size 1.229 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MCC_Library."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Emali: cgapbs-remail.nih.gov
Tissue Procurement ATCC
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602269966F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4357985
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http://image.llnl.gov
Plate: LLAM9995 row: d column: 18
High quality sequence stop: 591.
Location/Qualifiers
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100.0%; Pred. No. 1.2e-276;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:4357985"
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Matches 597; Conservative
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BF969043
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/issue_type="neuroblastoma"
/lab.host="DH10B (phage-resistant)"
/lab.host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: poTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by Oligo-dT priming. Directionally
cloned into ECORIXAhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NHLMGC Library."
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1 (bases 1 to 664)
NIH-MGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE383336 664 bp mRNA EST 21-JUL-2000 601298249F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3628308 5',
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Plate: LLCM313 row: a column: 13
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                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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100.0%; Pred. No. 2.9e-273;
ive 0; Mismatches 0;
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/db_xref="taxon:9606"
/clone="IMAGE:3628308"
/clone_lib="NIH_MGC_19"
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Location/Qualifiers
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Best Local Similarity 100.
Matches 590; Conservative
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/tissue_type="neuroblastoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Orden brain; Vector: poTB7; Site_1: XhoI; Site_2: BCORI; DNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAGGG). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tgocgtcattacggagaccaggtggacagggtcctgggcaccctggctgctgtgtttgtg 1632
                                                                                                                                                                                                                      aggagtgcgcaggacggcccagcccagcagagaaaagaagtcagtacccagaaatcatc 1452
                                                                                                                                                                                                                                                                                                                                                                                                              ttoottggaacagggtotgccatcccgatgaagattcgaaatgtcagtgccacacttgtc 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at: image.llnl.gov
High quality sequence stop: 600.
                                                                                                                                                                                                                                                                                                                                                               BE382353 692 bp mRNA EST 21-JUL-2000 601298656F1 NIH_MGC_19 Homo sapiens CDNA clone IMAGE:3629028 5'
                                                                                                                                                                                                                                                                                        Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 692)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                              1 ACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACAACCTTCGCAGCCACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     taccagctccgtcccaggaggagtggcagagggatgccattattacttgcaatcctgag
                                                                                                                                                                                                                                                                         gaattcatagttgaggcgctgcagcttcccaacttccagcagagcgtgcaggagtacagg
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/db_xref="taxon:9606"
/clone="IMAGE:3629028"
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1. .692
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BE382353.1 GI:9327718
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Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                 tgctactggactgtggtgagggcacatttgggcagctgtgccgtcattacggagaccagg 1594
                                                                  tocogatgaagattogaaatgtoagtgocacacttgtoaacataagcocogacacgtoto 1534
                                                                                                                                                                                                                                                                                                                                                                                               acaaccagtgccaggaggtcctgcaccacatcagtatgattcctgccaaatgcttcagg 1834
                                   Gaps
                                                                                cgcttcaccctttgctggtggttgccccaaccagctcaaagcctggctccagcagtacc
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                                  Indels
23.8%; Score 590; DB 10; L
100.0%; Pred. No. 2.9e-273;
ive 0; Mismatches 0;
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Primates;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
1 (bases 1 to 920)
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KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT

FEATURES

REFERENCE

DEFINITION

BE382353 LOCUS

ACCESSION VERSION

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BG756043
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                                                                                                                                                                                                                                                                                                                                    /tissue_type="adenocarcinoma cell line"
/Issue_type="adenocarcinoma cell line"
/Isb_host="NH10B (phage-resistant)"
/note="Organ: colon; Vector: poTB7; Site_1: XhoI; Site_2:
FOORI; CDNA made by oligo-dT priming. Directionally
Cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size=selected 500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
36 a 261 c 272 g 190 t l others
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                                                 Contact: Robert Strausberg, Ph.D.
Bmal: cgapbS-remail.nhin.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         441 TTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGGCGTGCAGGAGTACAGGAGG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501 AGTGCGCAGGACGCCCCAGCCCCAGCAGAAAGAAGTCAGTACCCCAGAAATCATCTTC 560
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1307 row: p column: 16
High quality sequence stop: 736.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 561; DB 11;
Pred. No. 2.8e-259;
0; Mismatches 0;
                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MGC_15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 22.6%;
Best Local Similarity 99.9%;
Matches 681; Conservative (
                                     Unpublished (1999)
                                                                                                                                                                                                                                                          1. .920
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   AUTHORS
                                                                                                                                                                                                                                        FEATURES
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/issue_type="primary B-cells from tonsils (cell line)"
/lab_host="primary B-celsstant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: porB7; Site_1: XhoI;
Site_2: EcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                         602716533F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856360 5', mRNA sequence.
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                                                                                                  ataagccccgacacgtctctgctactggactgtggtgagggcacatttggggcagctgtgc 1575
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 09
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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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100.0%; Pred. No. 7.2e-257;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: LLCM1707 row: b column: 09
High quality sequence stop: 878.
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/organism="Homo sapiens"
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/clone="IMAGE:4856360"
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Mammalia; Eutheria;
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Matches 556; Conservative
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Contact: Robert Strausberg, Ph.D.
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BG396395
BG396395.1 GI:13289941
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Mammalia; Eutheria;
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                                                                                                                                                                      Local
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., CDNA Library Preparation: M. Bento
Soares, Ph.D. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNE, send email to:
Info@linage.llnl.gov
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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/tissue_type="fibrotheoma"
/nb_most="DH108 (phage-resistant)"
/note="Organ: ovary; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI: 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7099f04.x1 NCI_CGAP_Ov18 Homo sapiens cDNA clone IMAGE:3644670 3' similar to TR:Q9V5J4 Q9V5J4 CG3298 PROTEIN. ;, mRNA sequence. BR434169 GI:11446441 EST.
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                                                          2286 gctgattcccccactgaaagccctgtttgctggcgacatcgaggagatggaggagggcg
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Location/Qualifiers
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Catarrhini; Hominidae;
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Pred. No. 2e-255;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4581700"
/clone="IMAGE:4581700"
/clone="IMAGE:16"
/lab_host="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="organ: eye; Vector: pOTBY: Site_1: XhoI; Site_2: Chote: Organ made by voligo-dT priming. Directionally cloned into Ecori/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM1302 row: n column: 05
High quality sequence stop: 779.
I. Cation/Qualifiers
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Matches 543; Conservative
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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="INAGE:4542553"
/clone="INAGE:4542553"
/clone="INAGE:4542553"
/clone=Lib="NHI-MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="Bh108 (phage-resistant)"
/note="Organ: placenta; Vector: pOTB); Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the birectionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAGG(5). Size-selected >500bp for average insert size 1:8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 614)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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602404708F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:4542553 5'
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can k
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1222 row: o column: 02
High quality sequence stop: 614.
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100.0%; Pred. No. 2.5e-244;
ive 0; Mismatches 0;
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nes 530; Conservative
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/cell_line="MGG3"
/lab_host="BH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2: ECORI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5 adaptor: GGCACAGGGG). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zab-coNA synthesis Att (Stratagene) and Superscript II RT (Life Technologies)."
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 761)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM802 row: p column: 14
High quality sequence stop: 761.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Maminalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 526)

1 (bases 1 to 526)

2 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

1 Unpublished (1997)

1 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michaell R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to:
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1; prostate cancer predisposing gene; HPC2; chromosome 17p; therapy; peptide therapy; drug design; ss.
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The present sequence is the coding sequence of the human prostate cancer predisposing gene HPC2, which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs. This sequence was isolated by cloning and sequencing the region of the genome which appeared to cause a predisposition to prostate cancer. (HPC)2 nucleic acids, polypeptides, and treatment and diagnosis of prostate cancer Page 98-100; 157pp; English (HPC)2 antibodies, useful for cancer prostate Claim 3; Human 

T; 0 other; 598 .; ö C; 848 707 A; 805 BP; 2958 Sequence

ö 540 099 120 240 360 410 480 530 590 009 720 780 180 230 290 420 650 accatategeaggeaccegeeegeegegageggeegegaaggaeeegetgeggeaeetg 170 atgtgggcgctttgctcgctgctgcggtccgcggccggacgcaccatgtcgcagggacgc 110 Gaps atgtgggcgctttgctcgctgctgctgcggtccgcggacgcaccatgtcgcagggacgc accatatcgcaggcacccgcccgccgcgaggggccgcgcaaggaccgctgcggcactg aaccggtatctcttcaactgtggagaaggcgttcagagactcatgcaggagcacaagtta gaaaggceteteagcaggeteagtecagagegatetteagaeteegagtegaatgaaaat cycacycyayayaaycygcyyaccytcyyyytyctccyycygcccaaacaccytytaccty caggtggtggcagcgggtagccggggactcgggcgccgccctacgtcttctccgagttc cctccacaactggaaaaatacctcgaagcaatcaaaatatttctggtccattgaaagga cetecacaactggaaaaatacetegaageaateaaaatattteteggteeattgaaagga atagaactggctgtgcgccccactctgccccagaatacgaggatgaaaccatgacagtt gtagettteatetgtaagetteaettaaagagagaaaettettggtgeteaaageaag cgcacgcgagagaagcgggaccgtcgggggtgctccgggcggcccaaacaccgtgtacctg ô Length Indels 21; ; 0 DB Score 2481; Pred. No. 0; ; Mismatches ; Query Match 100.0%; Best Local Similarity 100.0%; Matches 2481; Conservative 0; 241 Н 111 121 171 231 291 301 351 361 411 471 481 531 541 591 601 651 661 711 721 181 421 qq ò q οy g δy Dp Qγ QQ Ω Ω οy QQ Qy Db ÓΫ Db QΥ g οy Dp δ g δ οy

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replacing, repairing, or compensating for a DNA sequence within that
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| Qy<br>Dp                                                        | Qy<br>Db                                                        | Oy<br>Dp                                                             | Oy<br>Ob                                                    | Qy                                                             | Oy<br>Dp                                                         | Qy<br>Dp                                                       | Qy<br>Db                                                       | Qy                                                           | oy<br>Ob                                                      | Oy<br>Db                                                      | oy<br>og                                                    | Qy                                                               | Qy<br>Db                                                       | Qy<br>Db                                                         | Qy<br>Db                                                        | OY<br>Dp                                                         | Oy<br>Db                                                                                                    |

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29-JUL-1999; 99JP-0248036. 27-AUG-1999; 99JP-0300253. 11-JAN-2000; 2000JP-0118776. 02-MAY-2000; 2000JP-0183767. 09-JUN-2000; 2000JP-02418999.

(HELI-) HELIX RES INST

ij Yamamoto Ë Saito K, Otsuki ж, ashi K, Nagai K Hayashi I A, Naga: Wakamatsu , H Nishikawa T, Wakama Sugiyama Isogai T, ś Ota T, Ishii 9

WPI; 2001-318749/34

full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

Claim 8; SEQ ID 11557; 2537pp + CD ROM; English

The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comprises: (a) an oligo-dr primer and an oligonucleotide comprises one of
the complementary strand of a polyuucleotide which comprises one of
the 5602 nucleotide comprisines at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polyuucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polyuucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence of polyuucleotide which comprises a 1'-end sequence of more those defined in
complementary the primer sets is selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polyuucleotides,
the full-length cDNAs. The primers are also useful for the
cdetection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cC CNNAs easily without any specialised methods. AAH03616 to AAH13628 and
AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
crepresent oligonucleotides, all of which are used in the exemplification the present invention. 

C; 856 G; 601 T; 0 other; Sequence 2976 BP; 712 A; 807

1; atgtgggcgctttgctcgctgctgctgcggtccgcggacgcaccatgtcgcaggacgc 60 aaccggtatctcttcaactgtggagaaggcgttcagaagactcatgcaggagcacaagtta 3, Length 2976; Indels 22; DB Score 2022; DE Pred. No. 0; 0; Mismatches ; 81.5%; 99.8%; Conservative Query Match Best Local Similarity Matches 2412; Conserv 75 121 195 241 315 61 181 q g δy g ò g δ g ŏ

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KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; w anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; mimunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; kw hypotensive; dermatological; immunosuppressive; antitinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; kw antianemanic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; hypertension; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; kw cholestrool ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; kw bone damage; cartilage damage; antiinflammatory disease; coagulation; kw thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; catigorialic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; antidiabetic; and antianaemic. The sequences can be used for determining the presence of or predisposition to or preventing or treating the presence of our predisposition to or preventing or treating the presence of out predisposition associated with an ORFX associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy coetors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthitis, graft vs host disease, cardiovascular disease, diabetes mellitus, chylenatosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, alleaties, aplastic annemia, but wounds, bone and cartilage damage, nocturnal haemoglobinuria, antinificamenda as a contraceptive.
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                                                                                                                 Human ORFX ORF2000 polynucleotide sequence SEQ ID NO:3999
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05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                           RESULT
                                                                                                                                                  The present invention describes primer sets for synthesising 5602
full-length cDNAs defined in the specification. Where a primer set
comptises: (a) an oligo-dT primer and an oligouncleotide comptiementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises a 3'-end sequence complementary to the
oligonucleotide which comprises a 1'-end sequence, where the
oligonucleotide comprises a 1'-end sequence, where the
oligonucleotide comprises a 1'-end sequence, where the
oligonucleotide comprises as 1'-end sequence, where the
oligonucleotide comprises a 1'-end sequence, where the
oligonucleotide comprises of the abnormality of the full-length cDNAs. The primers are also useful for the
connection and/or diagnosis of the abnormality of the proteins encoded by
the full-length cDNAs. The primers allow obtaining of the full-length
cDNAs easily without any specialised methods. AAH33639 and
AAH13633 to AAH13642 represent human amino acid sequences; and AAH3639
crepresent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
0
                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accatatcgcaggcacccgcccgccgcgagcggccgcgcaaggacccgctgcggcacctg 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 accatatogcaggcaccogccogcogogagoggcogcaaggaccogctgcoggcacctg 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        caggtggtggcagcgggtagccgggactcgggccgcgctctacgtcttctccgagttc 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 aaccggtatctcttcaactgtggagaaggcgttcagagactcatgcaggagcacaagtta 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaggttgctcgcctggacaacatattcctgacacgaatgcactggtctaatgttggggggc 360
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                                                                                                               Yamamoto J;
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                                                                                                              Saito K, Y. Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 584 BP; 122 A; 166 C; 178 G; 115 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.7%; Score 364; DB 22; I
llarity 100.0%; Pred. No. 4.1e-168;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID 2670; 2537pp + CD ROM; English.
                                                                                                            Ota T, İsogai T, Nishikawa T, Hayashi K, S.
Ishii S, Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                          Nishikawa
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention.
                                                                        (HELI-) HELIX RES INST.
                                                                                                                                                               WPI; 2001-318749/34.
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                                                                                                      Isogai T,
                                                                                                                                                                                                                                                            full-length cDNAs
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Best Local Simi
Matches 364;
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Human; prostate cancer predisposing gene; HPC2; chromosome 17p; gene therapy; peptide therapy; drug design; ds.
                                                                           Human prostate cancer predisposing gene HPC2 genomic sequence.
                                                                                                                                                                                                                   /note= "this sequence contains introns"
/transl_except= (pos:23892..23895,aa:Glu)
910..1154
                                                                                                                                                                   Location/Qualifiers
BP
                                                                                                                                                                                                         "HPC2"
AAA60207 standard; DNA; 26664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /number= 10
13756..13868
/*tag= 1
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16278..16416
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18583..18701
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2878..12936
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15283..15378
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16498..16583
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20349..20445
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1925..1995
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3025..3089
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/*tag= g
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8186..8244
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                                                                                                                                           Homo sapiens
                                                 07-DEC-2000
                         AAA60207;
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1030 cgcacgcgagagagagcgcggaccgtcgggggtgctccggcggcccaaacaccgtgtacctg 1089
                                         Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer
Human; gene expression product; diagnosis; tumour; colon cancer; colorectal adenocarcinoma; cell line SW480; cell proliferation; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia; hyperplasia; ds.
                                                                                                                                                                                                                                                                                           Human colon cancer cell line SW480 cDNA clone SEQ ID NO:315.
                                                                                                                                                                                                      AAZ80231 standard; cDNA; 238 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-IB01062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0088801
                                                                                                                                                                                                                                                               07-APR-2000 (first entry)
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Catino IJ, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-087220/07
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                                                                                                                                1150 aaccggt 1156
                                                                                                   aaccggt 247
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Carroll E,
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                                                                                                                                                                                                                                   AAZ80231;
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                                                                                                                                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%; Score 247; DB 21; Length 26664; 100.0%; Pred. No. 7.4e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26664 BP; 6173 A; 6300 C; 6519 G; 7661 T; 11 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 108-122; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Teng DHF, Simard J,
                                                                                                                                                                                                                                                                                                                      /number= 24
26447..26452
/*tag= z
                                                                                                                                                        /number= 20
23973..24093
/*tag= v
                                                                                                                                                                                                                                   /*tag= w
/number= 22
25026..25170
                                                                                                                                                                                                                                                                                           /number= 23
25812..26036
/*tag= y
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23795..23895
                                                                                                                                                                                                                    24354..24432
                                            22879..22917
                                                                                     23045..23154
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                             'number= 17
                                                                       /number= 18
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P-PSDB; AAB07228.
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Best Local Simi
Matches 247; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                        polyA_signal
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                                             exon
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    exon
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Monahan JE;

Bushnell SE;

Astle JH, Burgess CC, bus rti A, Ford DM, Lewis ME,

Derti A,

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                                                                                  the human colorectal adenocationma (colon cancer) cell line SW480. The CDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The CDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia,
                                                                 AA279917 to AAZ80766 represent double stranded cDNA clones isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 238 BP; 55 A; 57 C; 69 G; 57 T; 0 other;
Claim 15; Page 258; 469pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100. Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                 dysplasia or hyperplasia.
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970 accatategeaggeaceegeeegegageggeegeegegeaaggaeeegetgeggeaeetg 1029

121 cgcacgcgagagaagcgcggaccgtcggggtgctccgggcggcccaaacaccgtgtacctg 180

accatatcgcaggcacccgcccgccgcagagcggccgcaaggacccgctgcggcacctg 120

61

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AAA60373 standard; cDNA; 23 BP.
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AAA60373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the coding sequence of the murine prostate cancer predisposing gene Mm. HPC2, the human homologue of which is found on chromosome 17p. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs.
/partial
/note= "this sequence contains no termination codon"
                                                                       Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
                                                                                                                                                                                         Murine prostate cancer predisposing gene HPC2 coding sequence.
                                                                                                                                                                                                            Mouse; prostate cancer predisposing gene; HPC2; gene therapy; peptide therapy; drug design; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 326 BP; 39 A; 104 C; 127 G; 56 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                               Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 151; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Tavtigian SV, Teng DHF, Simard J,
                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                  /product= "Mm.HPC2"
                                                                                                                                       BP.
                                                                                                                                    AAA60390 standard; cDNA; 326
                                                                                                                                                                                                                                                                                                                                                        99WO-US26055
                                                                                                                                                                                                                                                                                                                                                                          98US-0107468
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Best Local Similarity 100.(
Matches 26; Conservative
                                                                                                                                                                                                                                                                  .269
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                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAB07230
                                                                                                                                                                                                                                                                                                                      WO200027864-A1
                                                                                                                                                                        07-DEC-2000
                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                         05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                          06-NOV-1998;
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                                                                                                                                                       AAA60390;
236
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                                                                                                                    RESULT
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The present sequence is part of the coding sequence of a variant of the human prostate cancer predisposing gene HPC2, which is found on chromosome 17p. This variant has been designated 1641nsG. Some alleles of this gene cause a predisposition to cancer, particularly prostate cancer, this allele being an example of this. The HPC2 gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of cancer drugs. This sequence was isolated by mutation screening of the HPC2 gene in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                    Human prostate cancer predisposing gene HPC2 variant 1641insG (normal).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                  Human; prostate cancer predisposing gene; HPC2; chromosome 17p; gene therapy; peptide therapy; drug design; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.9%; Score 23; DB 100.0%; Pred. No. 0.4 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Simard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Page 63; 157pp; English.
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                                                                                                                                                                                                                                                                                                                             99WO-US26055.
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  (first entry)
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es 23; Conserv
                                                                                                                                                                                                                          WO200027864-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tavtigian SV,
                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                             05-NOV-1999;
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07-DEC-2000
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Gaps

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The present sequence is a primer used in the isolation of the human and murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human version of the gene is found on chromosome 17p. Some alleles cause a predisposition to cancer, particularly prostate cancer. This gene and its protein can be used in peptide and gene therapy for cancer patients, as well as being useful as diagnostic tools (both for cancer sufferers and those with a predisposition to the disease) and in the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesel; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monitoring differential expression of genes in filamentous fungal cell uses fluorescence-labeled nucleic acids isolated from the cells and a substrate of expressed sequence tags -
                                                                                                       Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies, useful for treatment and diagnosis of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multiple gene expression; filamentous fungal cell; EST;
                 Rommens JM;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 38 BP; 10 A; 9 C; 11 G; 8 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.8%; Score 20; DB
100.0%; Pred. No. 13;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusarium venenatum EST SEQ ID NO:1820.
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                    Simard J,
                                                                                                                                                                     Example 5; Page 59; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOVO ) NOVO NORDISK BIOTECH INC (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shuster JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF09297 standard; cDNA; 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 GACGCACCATATCGCAGGCA 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 gacgcaccatatcgcaggca
                    Teng DHF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
                                                          WPI; 2000-376481/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-594572/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                    Tavtigian SV,
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                                                                                                                                                                                                                                                                                                                                                                    cancer drugs.
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                                                                                                                                                                                                                                                                                                                   New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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human chromosome 17p; gene therapy; peptide therapy; drug design;
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                                                                                                                                                                                                                                    Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID 28639; 71pp + CD-ROM; English.
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                                                                                                    21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                  Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                          WPI; 2000-500381/45.
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nes 21; Conserv
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                                                                                                                                                                                          (GEST ) GENSET
                                                                                                                                             26-FEB-1999;
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                 EP1033401-A2
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Matches

δò 8 in filamentous fungal cells

Olsen PB;

Clausen IG,

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Gaps

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Indels

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The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is the coding sequence for one such transcription factor. The transcription factor may

Claim 1; Pages 570-571; 747pp; English.

be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper,

homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBs, zinc finger domains of type 2 CysZHis2, CCAAT box elements and MYB.

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the global expression of genes from FF cells allows the production of genes from FF cells allows the production of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway englated using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an armorm cDNA clones including elimination of redundancy as one spot on an armorm cDNA clones including elimination of redundancy as one spot on an increarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF11853 represents ESTs from Aspergillus of the present all specifically claimed in the present invention.
the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring
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Sequence 308 BP; 88 A; 56 C; 100 G; 63 T; 1 other;

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0.8%; Score 20; DB 21; Length 308;
                 0; Indels
                 Mismatches
         Pred. No
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                                    2353
       100.08;
                                                     30 ggaggagcgcagggagaagc 49
                                    ggaggagcgcagggagaagc
                 20; Conservative
      Local Similarity
Query Match
         Best Loc
Matches
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Pinus radiata transcription factor DNA sequence #481. BP AAC57035 standard; DNA; 457 (first entry) 25-JAN-2001 AAC57035; 13 AAC57035 RESULT

Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetqum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBS; zinc finger domain; type 2 Cys2His2; CCAAT box element; MYB; ss. 

Pinus radiata

40200053724-A2.

09-MAR-2000; 2000WO-US06112. 14-SEP-2000

99US-0266513. 99US-0149485. 11-MAR-1999; 8-AUG-1999;

Shenk MA, Glenn M; McGrath A, Wood M,

GENESIS RES & DEV CORP LTD. FLETCHER CHALLENGE FORESTS LTD.

(GENE-) (FLET-) WPI; 2000-579369/54

New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide

Sequence 19 BP; 4 A; 7 C; 3 G; 5 T; 0 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; prostate cancer predisposing gene; HPC2;
human chromosome 17p; gene therapy; peptide therapy; drug design;
PCR primer; sequencing primer; ss.
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100.0%; Pred. No. 12;
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Best Local Similarity
Matches 20; Conserv
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                                Gaps
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                                                                                                                                                                                                                                                                                                    Human; mouse; prostate cancer predisposing gene; HPC2;
human chromosome 17p; gene therapy; peptide therapy; drug design;
PCR primer; sequencing primer; ss.
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0.8%; Score 19; DB 21; Length 19; 100.0%; Pred. No. 39; tive 0; Mismatches 0; Indels
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                                                              257 actgtggagaaggcgttca 275
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                Best Local Similarity 100.0
Matches 19; Conservative
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Matches 19; Conservative
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   Query Match
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Description

Match Length DB

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AF304370 BC001939 BC001393 AF001392 AF308698 AF308694 AF304371S1 AF304371S1 AF304371S1 AF304371S1 AF308696 AF30431 AF105345 AC091560 AC019331 
U23796 Arabidopsis AF047031 Arabidops AB014516 Homo sapi AL009199 Streptomy AC003107 Human DNA

81.5 2976 67.2 2908 5.7 2908 5.7 721 1.9 2721 1.9 2721 0.9 105195 0.9 105195 0.9 105195 0.9 105195 0.8 148193 0.8 125403 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 196613 0.8 11733 0.8 11429 0.8 117338 0.8 114521 0.8 117338 0.8 117338 0.8 116539 0.8 116549 0.8 166394 0.8 166394 0.8 166394

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| GenCore version                                                                                                       | ·   | Result<br>No.        | Sco      |
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| Copyright (c) 1993 - 2000 Compugen Ltd.                                                                               |     |                      | 24       |
| OM nucleic - nucleic search, using sw model                                                                           |     | 0 m =                | 200      |
| Run on: April 1, 2002, 09:32:36 ; Search time 1802.89 Seconds (without alignments) 22702.163 Million cell updates/sec | Sec | 41000                | 3677     |
| Title: US-09-988-687-1 Perfect score: 2481 Sequence: 1 atgtgggggtttggtcgctagaaggtcagagccagtga 2481                    |     | 110                  | -1 m     |
| Scoring table: OLIGO_NUC Gapext 60.0                                                                                  |     | C 12<br>13<br>14     |          |
| Searched: 1472140 segs, 8248589755 residues                                                                           |     | C 16                 |          |
| Word size : 0                                                                                                         |     | c 18                 |          |
| Total number of hits satisfying chosen parameters: 2944280                                                            |     |                      |          |
| Minimum DB seq length: 0 Maximum DB seq length: 2000000000                                                            |     | 22<br>23<br>23<br>23 |          |
| Post-processing: Listing first 45 summaries                                                                           |     | 25                   |          |
| Database : GenEmbl:*                                                                                                  |     | c 27                 |          |
| 1: gp_oa:*<br>2: gb_htg:*                                                                                             |     | c 29                 |          |
| 3: gb_rn:*<br>4: gb_om:*                                                                                              | ,   | 30<br>31             |          |
| 5: gb_ov:*<br>6: gb_pat:*                                                                                             |     | 32<br>33             |          |
| 7: gb_ph:*<br>8: gb_p]:*                                                                                              |     | C 34                 |          |
| 9: da la                                                                          |     | c 36                 |          |
|                                                                                                                       |     | 38                   |          |
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| 13: gb_un:*<br>14: gb_vi:*                                                                                            |     |                      |          |
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| 30: em_htqo_hum:*                                                                                                     | •   | VERSION              | <b>z</b> |
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| 34: em_ntg_nv:*<br>35: em_ntg_rod:*                                                                                   |     |                      | ſ        |
| 1                                                                                                                     |     | AUTHORS              | RS       |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 2908)

Tavtigian, S. V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M., Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayanath, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Edhaffari, S., Gupfe, J.S., Hu, R., Iliev, D., Janeck, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J.,

AF304370 2908 bp mRNA PRI 23-FEB-2001 Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 mRNA, complete cds.

AF304370.1 GI:10880932

Homo sapiens

human.

ALIGNMENTS

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Lake City, UT 84108, USA
Location/Qualifiers
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Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.. A candidate prostate cancer susceptibility gene at chromosome Nat. Genet. 27 (2), 172-180 (2001)
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621. Location/Qualifiers
1. 2997
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg.R.
Direct Submission
Direct Submission
Stational Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                 Homo sapiens, putative prostate cancer susceptibility protein, clone MGC:4102 IMAGE:2820640, mRNA, complete cds. BC001939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory
DNA Starary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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61. .2541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
2461 AAGAAGGTCAGAGCCCAGTGA 2481
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BC001939.1 GI:12804972
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                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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TITLE
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BC001939
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2041 accetectgatacatgaageceaceetggaagatggtttggaagaaggaagcagtggaaaag
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| SRE                                                                           | 0;                                                                          |                                                            |                                         |                                                     |                                                              |                                                     |                                                       |                                                 |                                                   |                                                                |                                        |                                                                 |                                      |                                                              |                                                   |                                        |                                            |
| IPPLKALFAGDIEBMEERREKRELRQVRAALL<br>KVRAQ"<br>98 t                            | 9; DB 9; Length 2997;<br>0;<br>ches 2; Indels 0; Gaps                       | cogacocaccatgtcgcaggacgc 60<br>                            | gegeaaggaccegctgeggeacctg 120<br>       | cggcggcccaaacaccgtgtacctg 180                       | cgcgctctacgtcttctccgagttc 240                                | yagactcatgcaggagcacaagtta 300<br>                   | gacaacatattcctgacacgaatgcactggtctaatgttgggggc 360<br> | gcttccaaagtgtgtactttctgga 420<br>               | aatatttctggtccattgaaagga 480<br>                  | atacgaggatgaaaccatgacagtt 540<br>                              | gaaagcaccaaccatgcagagtcca 600<br>      | ttcagactccgagtcgaatgaaaat 660<br>                               | gaggggtcagggactcttccctggtc 720<br>   | aaacttcttggtgctcaaagcaaag 780<br>                            | teccateattgetgetgteaaggae 840<br>                 | ggctgaagagctgtgtactcctcca 900<br>      | agatgaaagcttcattcaacccatc 960<br>          |
| EKVGVAEDHMKVCFGDFPTWPKLI.<br>LAGGLEDGEPQQKRAHTEEPQAKK<br>40 a 806 c 853 g 59; | 95.9%; Score 2379;<br>larity 99.9%; Pred. No. C<br>Conservative 0; Mismatch | atgtgggcgctttgctcgctgctgcggtccgcggccggacgcaccatgtcgcag<br> | agcaggcaccgccgccgcgagcggcgcgcgcaag.<br> | gagagaagcgcggaccgtcggggtgctccggcggcccaaacaccgt;<br> | gtggtggcagcgggtagccgggactcgggcgcgcgctctacgtcttctccgagttc<br> | aaccggtatctttcaactgtggagaaggcgttcagagactcatgcag<br> | aaggttgctcgcctggacaacatattcctgacacg<br>               | gtggaatgattcttactttaaaggaaaccgggcttccaaagtg<br> | ctccacaactggaaaatacctcgaagcaatcaaaatattttctg(<br> | atagaactggctgtgcggcccactctgccccagaatacgaggatgaaccatgacagtt<br> | taccagatccccatacacagtgaacagaggaggg<br> | gaaaggeeteteageaggeteagteeagagegatetteagaeteegagtegaatgaaaa<br> | ccacaccttccacatggtgttagccagagaag<br> | gctttcatctgtaagcttcacttaaagagagagaacttcttggtgctcaaagcaaa<br> | gagatgggcctcccagttggacagctgccatcgctcccatcattg<br> | ggaaaagcatcaccatgaaggaagagagatttgg<br> | gtgetgettttgtggtggtagaatgtecagatgaaage<br> |
| VT 7.4                                                                        | atch<br>cal Simi<br>2479;                                                   | atgtggg<br>        <br> ATGTGGG                            | accatatege<br>                          | cgcacgc<br>       <br> CGCACGCC                     | cag<br>   <br>  CAG                                          |                                                     |                                                       | ttaa<br>    <br>TTAA                            | 0-0                                               |                                                                |                                        |                                                                 | gag<br>   <br>GAG                    | gta<br>   <br>GTA                                            |                                                   | 9 <b>–</b> 9                           | gatectg<br>          <br>GATCCTG           |
| BASE COUN                                                                     | Query M<br>Best Lo<br>Matches                                               | Oy 1<br>Db 61                                              | Qy 61<br>Db 121                         | Qy 121<br>Db 181                                    | Qy 181<br>Db 241                                             | Qy 241<br>Db 301                                    | Qy 301<br>Db 361                                      | Oy 361<br>Db 421                                | Oy 421<br>Db 481                                  | Qy 481<br>Db 541                                               | Oy 541<br>Db 601                       | Oy 601<br>Db 661                                                | Qy 661<br>Db 721                     | Qy 721<br>Db 781                                             | Oy 781<br>Db 841                                  | Oy 841<br>Db 901                       | Oy 901<br>Db 961                           |

| Qy   | 961  | tgagaatgccacctttcagaggtaccaaggaaaggcagatgccccgtggccttggt       |
|------|------|----------------------------------------------------------------|
| Dβ   | 2    | GTGAGAATGCCACCTTTCAGAGGTACCAAGGAAAGGCAGATGCCCCCGTGGCCTTGGTG    |
| Qy   | 1021 | acatggccccagcatctgtgcttgtggacagcaggtaccagcagtggatgga           |
| qa   | 1081 | TTCACATGGCCCCCAGCATCTGTGCTTGTGGACAGCAGGTACCAGCAGTGGATGGA       |
| Qy   | 1081 | aactgtgcctcagttcacaacctt 1                                     |
| QQ   | 1141 | TTGGGCCTGACACCCAGCACTTGGTCCTGAATGAGAACTGTGCCTCAGTTCACATTCACTT  |
| Qy   | 1141 | goagocacaagattcaaacocagctcaacctcatccacccggacatcttccccctgctc 1  |
| QQ   | 1201 | SCCACAAGATTCAAACCCCAGCTCAACCTCATCCACCCGGACATCTTCCCCCTGCTC      |
| Qy   | 1201 | ccagtitccgctgtaagaaggaggcccaccctcagtgtgcccatggttcagggtgaa 12   |
| qq   | 1261 | TCCGCTGTATAGAAGGAGGCCCCACCCTCAGTGTGTGTTTTAGGTTCAGGGTGAA 1      |
| QY   | 1261 | cctcaagtaccagctccgtcccagaggaagtggcagagggatgccattattact 132     |
| qq   | 1321 | SCCTCCTCAAGTACCAGCTCCGTCCCAGGAGGAGTGGCAGGGGATGCCATATTACT 13    |
| Qy   | 1321 | atcctgaggaattcatagttgaggcgctgcagcttcccaacttccagcagagcgtg 1     |
| QQ   | 1381 | GCAATCCTGAGGAATTCATAGTTGAGGCGCTGCAGCTTCCCAACTTCCAGCAGGCGTG 14  |
| Qy   | 1381 | aggagtacaggaggagtgcgcaggacggcccagcccagc                        |
| qa - | 1441 |                                                                |
| Qy   | 1441 | agaaatcatcttccttggaacagggtctgccatcccgatgaagattcgaaatgtcagt 1   |
| qq   | 1501 | GAAATCATCTTCCTTGGAACAGGGFCTGCCATCCCGATGAAGATTCGAAATGTCAGT 1    |
| Qy   | 1501 | cacacttgtcaacataagccccgacacgtctctgctactggactgtggtgagggcaca 15  |
| QQ   | 1561 | CCACACTTGTCAACATAAAGCCCCGACACGTCTCTGCTACTGGACTGTGGTGAGGGCACG 1 |
| Qy   | 1561 | gggcagctgtgccgtcattacggagaccaggtggacagggtcctgggcaccctggct 162  |
| ΩΩ   | 1621 | IGGGCAGCTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTT                       |
| Oγ   | 1621 | acctgcacgcagatcaccacacgggcttgccaagtatcttgctg 168               |
| qa   | 1681 | CTGTGTTTGTGTCCCACCTGCACGCAGATCACCACGGGCTTGCCAAGTATCTTGCTG 1    |
| Οy   | 1681 | agagaacgcocttggcatctttgggaaagccgcttcaccctttgctggtggttgcc 1     |
| qq   | 1741 | GGCATCTTTGGGAAAGCCGCTTCACCCTTTGCTGGTGGTTGCC 18                 |
| ΟŶ   | 1741 | ccaaccagctcaaagcctggctccagcagtaccacaaccagtgccaggaggtcctgca     |
| qq   | 1801 | SCCTGGCTCCAGCAG                                                |
| Qy   | 1801 | acatcagtatgattcctgccaaatgccttcaggaaggggctgagatctccagtcctg      |
| qq   | 1861 | CATCAGTATGATTCCTGCCAAATGCCTTCAGGAAGGGGCTGAGATCTCCAGTCCTGCA 19  |
| Qy   | 1861 | aaagattgattcgctgttgcgaacatgtgatttggaagagtttcagac               |
| QQ   | 1921 | TGGAAAGATTGATCAGTTCGCTGTTGCGAACATGTGATTTGGAAGAGTTTCAGACCTGT 19 |
| Οy   | 1921 | ggtgcggcactgcaagcatgcgtttggctgtgctggtg                         |
| ΩD   | 1981 | IGGTGCGCCACTGCAAGCATGCGTTTGGCTGTGCGTGCTGCTGCTCTGGCTGG          |
| QY   | 1981 | ggtctattccggggacaccatgccctgcgaggctctggtccggatggggaaagatgcc 20  |
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ilarity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
                                                                              /note="Vector: pOTB7"
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7022621.

Location/Qualifiers
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Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (01-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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BC004158 1 GI:13278770
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Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford,
Greene, Mark Ketteman and Anuradha Madan

        2401
        ggoggcctggaggatggggagcctcagcagagggcccacacagaggccacaggcc

        2461
        gGcgcccrgaggatgggagcctcagcagaggggccccacacagaggagccacagaggcc

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        GGCGCCTGGAGGARCCTCAGCAGAAAGGGGCCCCAAAAGGCC

                                                                                   2161 ACACACAGCACAACGTCCCAAGCCATCAGCGTGGGGATGCGGATGAACGCGGAGTTCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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/db_xref="LocusID:60528"
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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| Oy<br>Db       | 721          | gtagettteatetgtaagetteaettaaagagagaaettettggtgeteaageaaag 780<br>     |
| QY<br>Db       | 781<br>850   | gagatgggcctcccagttgggacagctgccatcgctccatcattgctgctgtcaaggac 840<br>   |
| QY<br>Dp       | 841<br>910   | gggaaaagcatcactcatgaaggaagagattttggctgaagagctgtgtactcctca 900<br>     |
| Qy<br>Db       | 901          | gatcctggtgctgcttttgtggtggtagaatgtccagatgaaagcttcattca                 |
| Qy             | 961          | tgtgagaatgccacctttcagaggtaccaaggaaaggcagatgccccgtggccttggtg 1020<br>  |
| Qy<br>Dp       | 1021         | gttcacatggccccagcatctgtgcttgtggacagcaggtaccagcagtggatgga              |
| Oy<br>Dp       | 1081         | tttgggcctgacacccagcacttggtcctgaatgagaactgtgcctcagttcacaacctt 1140<br> |
| Oy<br>Dp       | 1141         | egcagccacaagattcaaacccagctcaacctcatccaccggacatcttcccctgctc 1200<br>   |
| O <sub>Y</sub> | 1201         | accagtttccgctgtaagaaggaggcccacctcagtgtgcccatggttcagggtgaa 1260<br>    |
| Qy             | 1261<br>1330 | tgcctcctcaagtaccagctccgtcccaggaggagtggcagagggatgccattattact 1320<br>  |
| O.Y<br>Dp      | 1321         | tgcaatcctgaggaattcatagttgaggcgctgcagcttcccaacttccagcagagcgtg 1380<br> |
| Qy             | 1381         | caggagtacaggaggtgcgcaggacgcccagccccagcagaaagaa                        |
| Qy             | 1441         | ccagaaatcatcttccttggaacagggtctgccatcccgatgaagattcgaaatgtcagt 1500<br> |
| Q <sub>y</sub> | 1501         | gccacacttgtcaacataagccccgacacgtctctgctactggactgtggtgagggcaca 1560<br> |
| Qy<br>Dp       | 1561         | tttgggcagctgtgcgtcattacggagaccaggtggacaggtcctgggcacctggct 1620<br>    |
| Qy<br>Db       | 1621         | gctgtgtttgtgtcccacctgcacgcagatcaccacagggcttgccaagtatcttgctg 1680<br>  |

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AK001392 2976 bp mRNA PRI 22-FEB-2000
Homo sapiens cDNA FLJ10530 fis, clone NT2RP2000985.
AK001392.1 GI:7022621
AK001392.1 GI:7022621
Oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA, clone_llsnT2RP2 clone:NT2RP2000985.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Stogair., Ota.T., Hayashi.K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai.K., Sugano,S., Shiratori.A., Sudo,H.,
Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
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E (bases 1 to 2976)

Esgal,T, and Obsuki,T.

Direct Submission

Submitted (16-FEB-2000) to the DDBJ/EMBL/GenBank databases. Takao

Isogal, Helix Research Institute, Genomics Laboratory; 1532-3 Yana,

Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp,

Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.j
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SLGKPLHPLLVVAPNQLKAMLQQYYNQCQEVLHHISMIPAKCLQEGAEISSPAVERLI
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KVGVAFDHMKVCLGDFPTMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSREL
AGGLEDGSLSRSGPTQRSHRPRRSEPSEDLGDPELRRLCVFCPTHAPVSALLAGRS"
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ougawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K., Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K., Ishii,S., Kawai,Y., Saito,K., Yananoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T. WBDO human cDNA sequencing project
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/db_xref="taxon:9606"
/cell_line="NT2"
/cell_type="teratocarcinoma"
/clone="NT2RP2000985"
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                     AACCGGTATCTCTTCAACTGTGGAGAAGGCGTTCAGAGACTCATGCAGGAGCACAAGTTA
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| aggaattcatagttgaggcgctgcagcttcccaacttccagcagagcgtg 1.<br> | gaggagtgcgcaggcccagcccagcagagaaagagtcagtac 1.<br> | ttccttggaacagggtctgccatcccgatgaagattcgaaatgtcagt 1<br> |                               |                                  |                                      |                                |                            |                                      | atcagttcgctgttgcgaacatgtgatttggaagagtttcagacctgt 1<br> |                                   | 9gggacaccatgcctgcgaggtttggttcggatggggaaagatgcc 2,<br> | atacatgaagccaccctggaagatggtttggaagaggaagcagtggaaag 21<br> |                               |                                  | gagttgcctttgaccacatgaaggtctgctttggagactttccaacaatg 2:<br> | ttococcactgaaagcoctgtttgctggcgacatcgaggagatggaggag 2;<br> | goggagetgeggeagtgeggeggeeeteetgteeaggagetggea 2.<br> |
| gcaatcctg.<br>              <br>GCAATCCTG                 | caggagtaca<br>                                    | cagaaatcatc<br>                                        | ccacactt<br>                  | ttgggcag<br>        <br>TTGGGCAG | ctgtgttt<br>       <br>crGrGrr       | agagagaa<br>                   | ccaacca<br>                | ര — ∢                                | tggaaagattg<br>              <br>TGGAAAGATTG           | ggtgegg<br>           <br> GTGCGG | tggtctattcc<br>               <br>TGGTCTATTCC         | cctcctg<br>                                               | caca<br>     <br>  CACA       | gctgaac<br>          <br> CTGAAC | agaaagtgg<br>             <br>AGAAAGTGG                   | ccaagctga<br>                                             | gcagggagaa<br>                                       |
| 1321 to<br> <br> <br> 1392 TC                             | 1381 ca<br>1452 CA                                | 1441 cc<br>                                            | 1501 gc<br> <br> <br> 1572 GC | 1561 ti<br> <br> <br> 1632 T     | 1621 ge<br> <br> <br> <br> <br> <br> | 1681 ca<br> <br> <br>  1752 Ca | 1741 cc<br> <br> <br> <br> | 1801 ca<br> <br> <br> <br> <br> <br> | 1861 gf<br> <br> <br>  1932 G5                         | 1921 ctc<br>                      | 1981 g1<br> <br> <br>  2052 G5                        | 2041 ac                                                   | 2101 ac<br> <br> <br> 2172 AC | 2161 ato<br>  <br> 2232 ATO      | 2221 ga                                                   | 2281 CC<br>1<br>2352 CC                                   | 2341 cc<br>                                          |
| Qy<br>Dp                                                  | Qy<br>Dp                                          | Qy                                                     | Qy<br>Db                      | Oy<br>Db                         | Qy<br>Dp                             | Qy<br>Db                       | Qy<br>Db                   | Qy                                   | Qy<br>Dp                                               | Qy<br>Db                          | Qy<br>Dp                                              | Qy<br>Dp                                                  | Qy<br>Dp                      | Qy<br>Db                         | Qy                                                        | Qy<br>Db                                                  | Qy<br>Db                                             |

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SM pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 2908)

E Tavtigian, S.V., Simard, J., Teng, D.H.F., Abtin, V., Baumgard, M.,

Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P.,

Beck, A., Camp, N.J., Carillo, A.R., Chen, Y., Dayananth, P.,

Chaffari, S., Gupte, J.S., Hu, R., Illew, D., Janecki, T., Kort, E.N.,

Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J.,

Pederson, A., Prenn, B., Peterson, K.T., Reid, J.E., Richards, S.,

Schroeder, M., Smith, R., Snyder, S.C., Swedlund, B., Swensen, J.,

Thomas, A., Tranchant, M., Woodland, A.M., Labrie, F., Skolnick, M.H.,

Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.

A candidate prostate cancer susceptibility gene at chromosome 17p

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KREPSGCGGGPRTVYLQVYAGSRDSSAALVYPSERNKYLENGGEGIORMOERKLKV

ARLDAN FLTRAHWSWYNGGLSGMILTLKETGLPKCVLSGPPOLEKYLEAIKIFSFSCPLKG

IELAVRPHSAPEYEDETMTVYQIPIHSEQRRGKHQPWGSPERPLSRLSPERSSDSESN

BENPEHLHPRGVORRGVRDSSLVVAFICKLHLKRGMFLVLKAREMGLPVGTAALAA

AVKDGKSITHEGREILALBELCTPPDPGGAARVVVCCPDESFIQPICGRATFQRYGKAD

APVALVVHMAPESVLVDSRYQQWMERPGPDTQHLVLNENCASVHNLRSHKIGTQLNLI
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Tartigian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Illev, D., Janecki, T., Kort, E.N., Laity, K., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K.T., Reid, J.E., Richards, S., Tromas, A., Tranchant, M., Woodland, A.-M., Labrie, F., Skolnick, M.H., Neuhausen, S., Rommens, J. and Cannon-Albright, L.A.
Unpublished Control of human HPC2/ELAC2
                                                                                                                                                                                                                               27-FEB-2001
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/db_xref="taxon:9598"
1. .2481
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| BASE CORIGIN        | COUNT                                  | LIHEATLEDGLEEEAVEKTHSTTSQAISVGMRMNAEFIMLNHFSQRYAKVPLFSPNFN<br>EKVOVAFDHKVCFGDFATMPKLIPPLKALFAGDIEEMEERREKRELRQVRAALLSRE<br>LAGGLEDGEPQQKRAHTEEPQAKKVRAQ"<br>712 a 788 c 819 g 589 t |  |
|---------------------|----------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| Que<br>Best<br>Matc | Query Matc<br>Best Local<br>Matches 24 | Match 67.2%; Score 1667; DB 9; Length 2908; ocal Similarity 99.4%; Pred. No. 0; s 2417; Conservative 0; Mismatches 15; Indels 0; Gaps 0;                                            |  |
| Oy<br>Db            | н н                                    | atgtgggcgctttgctcgctgctgctgcggtccgcggccggacgcaccatgtcgcagggacgc 60<br>                                                                                                              |  |
| Qy                  | 61                                     | accatatogoagoaccogocogogogogogogoagoagoaccogotgogoacctg 120<br>                                                                                                                     |  |
| Qy<br>Db            | 121<br>121                             | cgcacgcgagagaagcgggaccgtcggggtgtcccggcggcccaaaccgtgtacctg 180<br>                                                                                                                   |  |
| Oy<br>Db            | 181<br>181                             | caggiggiggcagcagggactcgggactcggcccgcgctctaccgagttc 240<br>                                                                                                                          |  |
| Qy<br>Dp            | 241                                    | aaccggtatctcttcaactgtggagaaggcgttcagagactcatgcaggagcacaagtta 300<br>                                                                                                                |  |
| . da                | 301                                    | aaggttgctcgcctggacaacatattcctgacacgaatgcactggtctaatgttgggggc 360<br>                                                                                                                |  |
| Qy<br>Db            | 361<br>361                             | ttaagtggaatgattcttactttaaaggaaaccgggcttccaaagtgtgtactttctgga 420<br>                                                                                                                |  |
| Qy<br>Db            | 421                                    | cctccacaactggaaaatacctcgaagcaatcaaaatattttctggtccattgaaagga 480<br>                                                                                                                 |  |
| Qy<br>Db            | 481                                    | atagaactggctgtgcggcccactctgccccagaatacgaggatgaaaccatgacagtt 540<br>                                                                                                                 |  |
| Qy<br>Db            | 541                                    | taccagatccccatacacagtgaacagaggagggaaagcaccaacca                                                                                                                                     |  |
| Qy                  | 601                                    | gaaaggcctctcagcaggctcagtccagagcgatcttcagactccgagtcgaatgaaaat 660<br>                                                                                                                |  |
| Qy<br>Db            | 661<br>661                             | gagccacaccttccacatggtgttagccagagaagagggtcagggactcttccctggtc 720<br>                                                                                                                 |  |
| Qy<br>Db            | 721<br>721                             | gtagettteatetgtaagetteaettaaagagagagaaettettggtgeteaaageaaag 780<br>                                                                                                                |  |
| Qy<br>Db            | 781<br>781                             | gagatgggcctcccagttgggacagctgccatcattgctgctgtcaaggac       840                                                                                                                       |  |
| Oy<br>Dp            | 841                                    | gggaaaagcatcactcatgaaggaagattttggctgaagatgtgtactcctcca 900<br>                                                                                                                      |  |
| Οy                  | 901                                    | gatcctggtgctgcttttgtggtggtagaatgtccagatgaaagcttcattca                                                                                                                               |  |

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A candidate prostate cancer susceptibility gene at chromosome 17p 1175785
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    acctcctgatacatgaagccaccctggaagatggtttggaagaggaagcagtggaaaag
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| 540                                                           | 009                                             | 099                                                              | 720                                                             |                                                             | 840                                                          | 006                                                            | 096                                                   | 1020                                                             | 1080                                                     | 1140                                                         | ōō                                                             | 1260<br>1260                                                   | 1320                                                        | 1380                                                             | 1440                                                    | 1500                                                             | 1560                                                             |
|---------------------------------------------------------------|-------------------------------------------------|------------------------------------------------------------------|-----------------------------------------------------------------|-------------------------------------------------------------|--------------------------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------|------------------------------------------------------------------|----------------------------------------------------------|--------------------------------------------------------------|----------------------------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------------|------------------------------------------------------------------|---------------------------------------------------------|------------------------------------------------------------------|------------------------------------------------------------------|
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| 481                                                           | 541                                             | 601                                                              | 661                                                             | 721                                                         | 781                                                          | 841                                                            | 901                                                   | 961<br>961                                                       | 1021                                                     | 1081                                                         | 1141                                                           | 1201                                                           | 1261<br>1261                                                | 1321                                                             | 1381<br>1381                                            | 1441                                                             | 1501                                                             |
| Qy                                                            | Qy                                              | Qy                                                               | Qy<br>Db                                                        | Qy<br>Db                                                    | Qy                                                           | Qy                                                             | Qy                                                    | Qy                                                               | Qy                                                       | Qy                                                           | Qy                                                             | Qy                                                             | Qy                                                          | Qy                                                               | Qy<br>Db                                                | Qy<br>Db                                                         | Qy                                                               |

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AC005277 118788 bp DNA PRI 23-JUL-1998 Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence. AC005277
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118788)
Birren, B., Fasman, K., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone hRPK.597_M_12
Unpublished
2 (bases 1 to 118788)
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AC005277
LOCUS
DEFINITION
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KEYWORDS
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AUTHORS
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| AUTHORS Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boatin, C., Boutwell, C., Brown, A., Castle, A., Cerny, J., Cooke, P., Depayre, E., Devon, K., Dewar, K., Donelan, E., Etemadi, S., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Genshaimer, S., Geraigery, K., Gilmartin, T., Grant, G., Hagos, B., Harris, K., Horton, L., Howland, J.C., Hui, L., Jacotot, L., Kan, L., Madonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Machman, A., Nahi, R., Naplor, J., Niloff, M., O'Connor, T., Pavlin, B., Peterson, K., Rieley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Strickland, C., Subramanian, A., Torruella Miller, I., Vassillev, H., Vo, N., Wagner, A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and | TITLE Direct Submission  JOURNAL Submitted (10-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  RESERRICE 3 (bases 1 to 119788)  RUTHORS Birren,B., Fasman,K., Linton,L., Nusbaum,C., Lander,E., Allen,N., Barker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Boatin,C., Butwell,C., Brown,A., Castle,A., Cerny,J., Cooke,P., Depayre,E., Devon,K., Dewar,K., Donelan,L., Etemadi,S., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Gardyna,S., Gensbeimer,S., Geralgery,K., Gilmartin,T., Grant,G., Hagos,B., Harris,K., Horton,L., Howland,J.C., Hui,L., Jacotot,L., Kann,L., Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K., Maldarim,J., Molla,M., Morris,M., Morris,M., Morris,M., Morris,M., Morris,M., Roberts,D., Wolconor,T., Pavlin,B., Peterson,K., Riley,R., Roberts,J., Niloff,M., O'Connor,T., Pavlin,B., Strickland,C., Subramanian,A., Torruella-Miller,I., Vassiliev,H., Vo.A., Waqner,A., Wang,B., Wheeler,J., Wu,Y., Ye,W.J., Zhao,J., and | TITLE Direct Submission JOURNAL Submission JOURNAL Submission JOURNAL Submission JOURNAL Submitted (23-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 23, 1998 this sequence version replaced gi:3335015. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Only the first 118.8 kilobases of this clone are being submitted. The remainder overlaps accession number AC005274 (WICGR project | FEATURES Liston Coatlaps accession number AC005274 (WICGR project Liston) Location/Qualifiers Location/Qualifiers  / Liston Sapiens" / Clone   Homo sapiens" / Clone   Lib** RPCI-11 human BAC library" / Clone   Lib** RPCI-11 human BAC library" / Chomosome = "17" / Complement (318 . 3821) / Chomosome = "17" / Complement (418 . 3821) / Chomosome = "17" / Complement (418 . 3821) / Chomosome = "17" / Complement (418 . 3821)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

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Tavtigian, S. V., Simard, J., Teng, D. H. F., Baumgard, M., Beck, A., Cantilo, A. R., Chen, Y., Dayananth, P., Desrochers, M., Cantilo, A. R., Chen, Y., Dayananth, P., Desrochers, M., Dumont, M., Farnham, J. M., Frank, D., Frye, C., Ghaffari, S., Gupte, J. S., Hu, K., Illev, D., Janecki, T., Kort, E. N., Lairy, K. E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K. T., Redlud, J. E., Richards, S., Schroeder, M., Smith, R., Woodland, A. M., Labrie, F., Skolnick, M. H., Neuhausen, S., Rommens, J. and Cannon-Albright, L. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission Submitselon Submitted (12-SEP-2000) Myriad Genetics, Inc., 320 Wakara Way, Salt Lake City, UT 84108, USA Location/Qualifiers
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HPC2/ELAC2"
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                                                                                                                                                                                                                                                                                                             A strong candidate prostate cancer susceptibility gene at chromosome 17\,p
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                                                              Homo sapiens
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                                                                                                                                                                                                                                        (bases 1 to 721)
Tavitidian, S. V., Shmard, J., Teng, D. H. F., Baumgard, M., Beck, A.,
Tavitidian, S. V., Shmard, J., Teng, D. H. F., Baumgard, M., Beck, A.,
Camp, N. J., Carillo, A. R., Chen, Y. Dayananth, P., Desrochers, M.,
Gupte, J. S., Hu, R., Illev, D., Janecki, T., Kort, E. N., Laity, K. E.,
Leavitt, A., Leblanc, G., McAtthur-Norrison, J., Pederson, A., Penn, B.,
Snyder, S. C., Swedlund, B., Swensen, J., Thomas, A., Tranchant, M.,
Moodland, A. M., Labrie, F., Skolnick, M. H., Neuhausen, S., Rommens, J.,
and Cannon-Albright, L. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johann J. Carillo, A. R., Chen, Y., Baumgard, M., Beck, A., Cavilgian, S.V., Simard, J., Teng, D.H.F., Baumgard, M., Beck, A., Camp, N. J., Carillo, A.R., Chen, Y., Dayananth, P., Desrochers, M., Bumont, M., Farnham, J.M., Frank, D., Frye, C., Ghaffari, S., Gupte, J.S., Hu, R., Ilkew, D., Janecki, T., Kort, E.N., Laity, K.E., Leavitt, A., Leblanc, G., McArthur-Morrison, J., Pederson, A., Penn, B., Peterson, K. T., Reid, J.E., Richards, S., Schroeder, M., Smith, R., Snyder, S.C., Swellund, B., Swensen, J., Thomas, A., Tranchant, M., and Cannon-Albright, L.A.
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/product="putative prostate cancer susceptibility protein
HPC2/ELAC2"
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                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db.xref="G1:10880930"
/translation="EQRRGKHQPWGSPRPLSRLSPERSSDSESNENEPHLPH"
143 c 184 g 193 t
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                AF304371S1 721 bp DNA PRI 19-OCT-2000 Homo sapiens putative prostate cancer susceptibility protein HPC2/ELAC2 gene, exon 7 and partial cds.
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/organism="Homo sapiens"
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GGPNTVYLQVVAAGGRDAGAALKVFSEYNRYLFNCGEGVQRLMQEHKLKVARLDNIFL
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GGPNTVYLQVVAAGGRDAGAALYVFSEYNRYLFNCGEGVQRLMQEHKLKVARLDNIFL
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DSSAGANRKAMGRDPSLVVAFVCKLHLRKGNFLVLKAKELGLPVGTAAIAPIIAAVKD
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FPQLTSFYSKEGSTLSVPTVRGECLLKYQLRFREWQNDTTLDCNTDEFIABALELP
STOBSVBEYRNVQENPAPAEKRSQY PEIVFLGTRETBMKIRNVSSTLVNLSPDKSV
LLDCGEGTFGQLCRHYGQQIDRVLCSLTAVFVSHLHANHHTGLINILLQREHALASLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative prostate cancer susceptibility protein"
join(<8470. 8600,9077. 9127,9266. 9336,948. .10012,
10957. .11014,12096. .12164,12933. .13064,14902. .14960,
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27291. .21677,21757. .21842,23553. .23671,24619. .24715,
28731. .22429,27763. .27801,27930. .28039,28553. .28652,
28733. .28853,29101. .29179,29710. .29854,30406. .30624,
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/protein_id="AAK29420.1"
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/product="putative prostate cancer susceptibility protein"
<8470. .>31277
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                                             /db_xref="taxon:10090"

join(<8470. 8690.9077. 9127,9266. 9336,9948. 10012.

join(<8470. 8690.9077. 9127,9266. 13064,14902. 14960.

16609. 16667.16746. 16818,17370. 17482,18671. 18766.

21539. 21677,21757. 21842,23553. 23671,24619. 24715.

27291. 27429,27763. 27801,27930. 28039,28553. 28652,

28733. 28833,29101. 29179,29710. 29884,30406. >30639)
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10957. _11014,12096. _12164,12933. _13064,14902. _14960,
16609. _16667,16746. _16818,17370. _17482,18671. _18766,
21539. _21677,21757. _21842,23553. _23671,24619. _24715,
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28733. _28853,29101. _29179,29710. _29854,30406. _30639,
/gene="Elac2"
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join(8470. 8690,9077. 9127,9266. 9336,9948. 10012,
10957. 11014,12096. 12164,12333. 13064,14902. 14960,
16609. 16667,16746. 16818,17370. 17482,18671. 18766,
21539. 21677,21757. 21842,23553. 23671,24619. 24715,
27291. 27429,27763. 27801,27930. 28039,28553. 28652,
28733. 28853,29101. 29179,29710. 29854,30406. 30624,
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KPEQPLLVVARTQLAMLQQYHNHCQEILHHYSMIPAKCLQKGAEVSNTTLERLISLL
LETCDLEEFGYCLVRHCKHAFGCALVHSGWKWVYSGDTMPCEALVQMKDATLLIHE
ATLEDGLEEEAVEKTHSTTSQAINVGMRMNGFIMINHFSQRYAKIPLFSPDFBKVG
IAFDHMKVCFGDFPTVPKLIPPLKALFAGDIEEMVERREKRELRLVRAALLTQQADSP
                                                                                                                                                     /product-"ELAC2"
/protein_id="AA624918.2"
/brotein_id="A1924918.2"
/brotein_id="I1992348.2"
/branslation="MAALRSLLEPLGLRTMSOGSARRPRPSKDPLRHLRTREKKGPGPGPTAINSTYLEPLOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFERTOFFER
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SAPEYKDETWTVYQVPIHSERRCGKQQPSQSPRTSPNRLSPKQSSDSGSAENGQCPPE
DSSAGANRKAWGRDPSLVVAFVCKLHLRKGNFLVLKAKELGLPVGTAAIAPIIAAVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKSITYEGREIAAEELCTPPDPGLVFIVVECPDEGFILPICENDTFKRYGAEADAPVA
LVHTAAPEVLJDSKYQMRERGPDTOHLILNBROESVHNIASHKIOTYGLSILPPDI
LPPDI PROFTSFYSKEEGSTLSVPYREGECLLKYQLRSKREWQRDTTPDCNTDEFIAEALELP
SPQESVEEYRKNVQENAPAEKRSQYPEIVFLGTGSALPMKIRNVSSTLVNLSPDKSV
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Submitted (09-FEB-2001) Myriad Genetics, Inc., 320 Wakara Way, Salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                         Homo sapiens HPC2/ELAC2'
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741 c 748 g 564 t
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Unpublished
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1. .34593
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1 (bases 1 to 41514)

1 Lamerdin,J.E., McCready,P.M., Skowronski,E., Adamson,A.W., Burkhart-Schultz,K., Gordon,L., Kyle,A., Ramirez,M., Stilwagen,S., Phon,H., Velasco,N., Do,L., Regala,W., Terry,A., Garnes,J., Danganan,L., Poundstone,P., Christensen,M., Georgescu,A., Avila,J., Liu,S., Attix,C., Andreise,T., Trankhelm,M., Amico-Keller,G., Kromiller,B., Arellann,A., Montgomery,M., Ow,D., Nolan,M., Trong,S., Kobayashi,A., Olsen,A.S. and Carrano,A.V. Sequence analysis of a 3.5 Mb contig in human 19913.3 containing a serine procease gene cluster
                                             ATLEDGLEEEAVEKTHSTTSOAINVOMRMNAEFIMLNHFSORYAKITELFSPDENEKVG
IAFDHMKVCFGDFPTVPKLIPPLKALFAGDIEEMVERREKRELRLVRAALLTQQADSP
EDREPQQKRAHTDEPHSPQSKKESVANTLGARV"
KPFQPLLVVAPTQLRAWLQQYHNHCQEILHHVSMIPAKCLQKGAEVSNTTLERLISLL
LETCDLEEEFQTCLVRHCKHAFGCALVHSSGWKVVYSGDTMPCEALVQMGKDATLLIHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (03-SEP-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Mational Laboratory, 7000 East Ave., Livermore, CA 94551, USA Mational Laboratory, 7000 East Ave., Livermore, CA 94551, USA Mational Laboratory, Cosmid R26660 (AC005328) to the left from bases 1 to 4.683 of this accession, and overlaps cosmid F8682 (AC005257) to the right from bases 41,662 to 43,514. Additional chromosome 19 map and sequence information may be obtained at:

Location/Qualifiers

1. 43514
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Submitted (27-AUG-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
3 (bases 1 to 43514)
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chromosomes from hybrid 5HL2-B, which carries chromosome
19 as its only human chromosome."
46. .152
                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA PRI 03-SEP-1998
19, cosmid R26634, complete sequence.
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/cell_line="5HL2-B"
/clone_lib="LL19NC03 R chromosome 19-specific cosmid
library"
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                                                                                                                                                                                                                      Length 34593;
                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                             1.9e-14;
                                                                                                                                                                                                                      1.9%; Score 46; DB 10;
                                                                                                                         9780 t
                                                                                                                                                                                                                                          100.0%; Pred. No. 1.9 cive 0; Mismatches
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/clone="R26634"
                                                                                                                    8142 g
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Best Local Similarity 100.(
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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/coun_ackerperimental
/prodence=not_experimental
sapiens cDNA clone 782260 3'; (391. .340); 100% identity.~(111. .152) AA609572 af15c02.s1 Soares testis NHT
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LSCFVTPDLARDLANDIMTLMSHTKPYIRKKALIEPLTNLIHSTSAMSLLYECVNTVI
AVLISLSSGMPNHSASIQLCVQKLRILIEDSDQNLKYLGLLAMSKILKTHPKSVQSHK
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complement(join(1296 .3391,9810 .9889,10209 .10330,
1096. 11081,11259 .11347,11830 .12019,12408 .12455,
12802 .12951,13883 .14054,14659 .14356,15248 .15425,
15871 .15944,16342 .16541,16661 .16736,17330 .17401,
17728 .17869,1845 .18490,19724 .19555,21385 .22215,
22266 .22434,22857 .23002,24481 .24529,24953 .25002,
28275 .28234,3013 .30244,31625 .31660,33594 .33701,
38134 .38214,38850 .38930,39742 .>39837)

//note="vesicle coat component, similar to alpha and gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="DDS similarity to overlapping ESTS:
AA431731 zw77903.s1 Soares testis NHT Homo saplens CDNA
clone 782260 3'; (339..11); 99% identity.-AA609572
af15c02.s1 Soares testis NHT Homo saplens cDNA clone
1031714 3'; (330..5); 99% identity.-AA448181 zw83c05.s1
Soares testis NHT Homo saplens cDNA clone 78258.84; (336..4); 99% identity.
                                                                        Homo sapiens cDNA clone 1031714 3'; (372. .331); 100% identity."
                                                                                                                                                                                                                                                                           /note="DDS similarity to overlapping ESTs: (608. .273) T05239 EST03128 Homo sapiens cDNA clone HFBCT75. Score: 621 Identity: 325/337 (96%).-(718. .3 AA46009 zv72a03.s1 Soares total fetus ND2HF8 9w Homo sapiens cDNA clone 759148 3'; Score: 755 Identity: 398/408 (97%)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Hypothetical human protein with no significant similarity to known proteins"
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Score: 744 Identity: 418/440 (95%). ~Additional EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="AP-3 complex delta subunit, partial CDS"
/protein_id="AAC34214.1"
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/note="Human AP-3 complex delta subunit mRNA"
                                                                                                                                                                                                                         complement(273. .608)
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2 (bases 1 to 105490)
Schudy, A., Blechschmidt, K., Schillhabel, M., Baumgart, C., Menzel, U.,
Weber, J., Schattevoy, R. and Rosenthal, A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bassa: 1 to 103490)
Schilhabel, M.B., Baumgart, C., Blechschmidt, K., Dette, M., Jahn, N., Lehmann, R., Menzel, U., Polley, A., Reichwald, K., Schudy, A., Siddiqui, R., Taudien, S., Wen, G., Schlegelberger, B., Slebert, R., Chromosome & genomic sequence
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HOMCO Sapiens Chromosome 8 clone RP11-104D16 map 8, WORKING DRAFT
SEQUENCE, 2 ordered pieces.
AC091560 GI:14626327
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                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* Location/Qualifiers
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                                                                                                  0.9%; Score 23; DB 9; Length 43514;
100.0%; Pred. No. 0.46;
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/clone="CTA-392C11"
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/organism="Homo sapiens"
/db_xref*"taxon:9606"
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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/rpt_family="Aluy"
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EKDYPWEKKSKRKKKKKEKKHKEKERDKKKKEREKKKSPKKKKHREKERETRKG
KKSKQPPGSEEAAGEPVQNGAPEEDQLPSSSYSLAENSYVKMTCDIRGSLOEDSO
VTVAIVLENRSSSILKGMELSVLDSLANRMARPQGSSVHDGVPVPFQLPGVSNRAQY
                                         IDICSQSNYQYITNFEWYISILVELTRLEGTRHGHLIAAQMLDVAIRVKAIRKFAVSQ
MASALLDSAHLLASSYQRRGICEVLYRAAMICGERSEHLQEPHTLLEAMLRPRYTLLEG
HIQAVYQNVVKLYASILQOKGAGFABGRQANYQLLYDRLPGFYQSADLEVQBRASC
ILQLVKHIQKLQAKDVPVABEVSALFAGELNVAPKAQKKVPVPEGLDLDAWINEPLS
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FNIIEVWSASKFTFKRIGYLAASQSFHEGTDVIMLTTNQIRKDLSSPSQYDTGVALTG
LSCFVTPDLARDLANDIMTLMSHTKPYIRKKAVLIMYKVFLKYPESLRPAFPRLKEKL
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ESGDLSMSSIKVDGIRMSFQNLLAKICFHHHFSVVERVDSCASMYSRSIQGHHVCLLV
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/protein_id="AAC34212.1"
/db_xref="GI:3478639"
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/rpt_family="MER9"
6938, .7227
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/rpt_family="(TAAA)n"
3908. .4090
/rpt_family="AluSq"
4101. .4266
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255. .7402
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/rpt_family="Alusg"
3570. .3866
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complement(5793..6
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/db\_xref="taxon:9606"

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                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 bp 190195; contig of 123832 bp in length. Location/Qualifiers
                                                     1 (bases 1 to 190195)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 8, clone RP11-104D16
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           provided by the submittor.
This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L11660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66264 66363; gap of 66364 190195; cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
                       Homo sapiens
                                                                                       Unpublished
                      ORGANISM
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/organism="Homo sapiens"

source

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 190705)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG 07-JUL-2000 Homo sapiens chromosome 8 clone RP11-104D16, WORKING DRAFT SEQUENCE, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7717162
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                                                                                                                                                                                                                                                                                                                    109 others
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Chemistry: Dye-terminator Big Dye; 51% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 182645 bases at least Q40
Consensus quality: 186230 bases at least Q30
Consensus quality: 186612 bases at least Q30
Insert size: 199000; agarose-fp
Insert size: 189205; sum-of-contigs
/chromosome="8"
/map-"8"
/clone="RP11-104D16"
/clone_lib="RPC1-11 Human Male BAC"
1. .66263
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
0.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.9%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.4 Matches 23; Conservative 0; Mismatches
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                                                                                                                                                                                vector_side:left"
66364._190195
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a 36687 c 36123 g
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2 (bases 1 to 190705)
Waterston, R.H.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                   9: gap of unknown length
1: contig of 19899 bp in length
1: gap of unknown length
1: contig of 21894 bp in length
1: gap of unknown length
1: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                           3 152228: contig of 27576 bp in length 9 152228: gap of unknown length 9 190705: contig of 38377 bp in length.
                                                           bp in length
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bp in length
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of 15209 bp in length
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of 7682 bp in length
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of 1641
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